

Sequence 7, Appli
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Sequence 14, Appli
Sequence 9, Appli
Sequence 10, Appli

28 690.5 54.6 238 3 US-09-005-299-7
29 690.5 54.6 238 3 US-09-515-431-7
30 690.5 54.6 263 2 US-08-768-964-2
31 690.5 54.6 263 3 US-09-005-299-2
32 690.5 54.6 263 3 US-09-515-431-2
33 676 53.5 229 3 US-08-833-488B-24
34 676 53.5 253 3 US-08-833-488B-20
35 587.5 46.5 227 1 US-07-869-933-14
36 587.5 46.5 227 3 US-09-103-663-14
37 576.5 45.6 222 1 US-07-869-933-12
38 576.5 45.6 222 3 US-09-103-663-28
39 576.5 45.6 222 3 US-09-103-663-28
40 576.5 45.6 222 3 US-09-103-663-28
41 570 45.1 201 3 US-09-015-734-12
42 570 45.1 201 4 US-09-515-311-12
43 522 41.3 199 3 US-08-833-488B-14
44 517 40.9 431 4 US-03-592-988C-9
45 517 40.9 435 4 US-03-592-988C-10

ALIGNMENTS

RESULT 1
US-07-869-933-13
; Sequence 13, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FcRI alpha subunit
US-07-869-933-13

Query Match 100.0%; Score 1264; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VPOKPKVSLNPPNRRIFKGENVTLTCNGNFFVSTKMFHNGSLSEETNSLNIYNAKF 60

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OM protein - protein search, using sw model
Run on: October 6, 2004, 08:59:40 ; Search time 15.1422 Seconds
(without alignments)
790.984 Million cell updates/sec

Title: US-10-763-400-6
Perfect score: 1264
Sequence: 1 VPOKPKVSLNPPNRRIFKGE.....RTRKGFRLLNPPKPKPKNN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1264	100.0	232	1	US-07-869-933-13
2	1264	100.0	232	2	US-08-756-387B-6
3	1264	100.0	232	3	US-09-103-663-13
4	1264	100.0	232	4	US-09-285-873-6
5	1264	100.0	232	4	US-09-944-277A-6
6	1264	100.0	257	1	US-07-869-933-11
7	1264	100.0	257	3	US-08-756-387B-2
8	1264	100.0	257	4	US-09-103-663-11
9	1264	100.0	257	4	US-09-285-873-2
10	1264	100.0	257	4	US-08-897-956A-1
11	1264	100.0	257	4	US-09-944-277A-2
12	991	78.4	978	4	US-08-897-956A-3
13	947	74.9	172	2	US-08-756-387B-13
14	947	74.9	172	4	US-09-285-873-13
15	947	74.9	172	4	US-09-245-764-9
16	947	74.9	172	4	US-09-944-277A-13
17	947	74.9	197	2	US-08-756-387B-11
18	947	74.9	197	4	US-09-285-873-11
19	947	74.9	197	4	US-09-944-277A-11
20	941	74.4	197	3	US-08-788-954-2
21	938	74.2	193	2	US-08-765-536-1
22	938	74.2	193	5	PCT-US95-08401-1
23	785.5	62.1	236	3	US-09-015-734-7
24	785.5	62.1	236	4	US-09-515-311-7
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Db 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
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Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 2
US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-6

Query Match 100.0%; Score 1264; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
Db 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
QY 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
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Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 3
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinnet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-13

Query Match 100.0%; Score 1264; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
Db 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
QY 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSEYKCOHQVNESEPVYLEVPSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
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Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 4
US-09-285-873-6
; Sequence 6, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Igs
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
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SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: NO. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-6

Query Match 100.0%; Score 1264; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPWNRIKGENVTLCNGNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 1 VPQKPKVSLNPWNRIKGENVTLCNGNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDFMLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDFMLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
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DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180
QY 181 FPIPLVLLFAVDITGLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232
DB 181 FPIPLVLLFAVDITGLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232

RESULT 5
US-09-944-277A-6
Sequence 6, Application US/09944277A
Patent No. 6682894
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

Query Match 100.0%; Score 1264; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPWNRIKGENVTLCNGNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 1 VPQKPKVSLNPWNRIKGENVTLCNGNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDFMLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDFMLLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180
DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180
QY 181 FPIPLVLLFAVDITGLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232
DB 181 FPIPLVLLFAVDITGLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232

RESULT 6
US-07-869-933-11
Sequence 11, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-869-933-11

Query Match          100.0%; Score 1264; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60
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QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
DB 206 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257

RESULT 7
US-08-756-387B-2
; Sequence 2, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-2

Query Match          100.0%; Score 1264; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 60
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QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
DB 206 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257

RESULT 8
US-09-103-663-11
; Sequence 11, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; EARLIER FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 257
; TYPE: PRI
; ORGANISM: Homo sapiens
; US-09-103-663-11

Query Match          100.0%; Score 1264; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSLNIVNAKF 85
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 232
DB 206 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNPKNN 257

RESULT 9
US-09-285-873-2
; Sequence 2, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
```



```

; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-2

Query Match 100.0%; Score 1264; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQPKVSLNPPNRIKGENVTITCNGNFFEVSTKWFHNGSLSEETSSLNIVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDSGEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKYWNHNISITNATVEDSGTYICTGKWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKYWNHNISITNATVEDSGTYICTGKWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNKPN 232
DB 206 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNKPN 257

RESULT 11
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-944-277A-2

; SEQ ID NO 1
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-08-897-956A-1

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Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 86 EDSGEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
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DB 146 YKDGALKYWNHNISITNATVEDSGTYICTGKWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNKPN 232
DB 206 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHKPNKPN 257

RESULT 10
US-08-897-956A-1
; Sequence 1, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
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Query Match 100.0%; Score 1264; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 7.4e-115; Indels 0; Gaps 0;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGNVTLTCGNNPFVSTKWFHNGSLSEETNSSLNIVNAKF 60
 DB 26 VPQPKVSLNPPWNRIFKGNVTLTCGNNPFVSTKWFHNGSLSEETNSSLNIVNAKF 85
 QY 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOASAEVWVEGQPLFLRCHGRNWDVYKVIY 120
 DB 86 EDGSEYKCOHQVNESEPVYLEVFSDDLLOASAEVWVEGQPLFLRCHGRNWDVYKVIY 145
 QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 180
 DB 146 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 205
 QY 181 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGRFLLNPHPKPNPKN 232
 DB 206 FPIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGRFLLNPHPKPNPKN 257

RESULT 12

US-08-897-956A-3
 ; Sequence 3, Application US/08897956A
 ; Patent No. 6423512
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Ellen Digan
 ; APPLICANT: Philip Lake
 ; APPLICANT: Hermann Gram
 ; TITLE OF INVENTION: Fusion Polypeptides
 ; FILE REFERENCE: 600-7244/CPA
 ; CURRENT APPLICATION NUMBER: US/08/897,956A
 ; CURRENT FILING DATE: 1997-07-21
 ; PRIOR APPLICATION NUMBER: 60/022,689
 ; PRIOR FILING DATE: 1996-07-26
 ; NUMBER OF SEQ ID NOS: 38
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 ; LENGTH: 978
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion polypeptide
 US-08-897-956A-3

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 QY 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOASAEVWVEGQPLFLRCHGRNWDVYKVIY 120
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RESULT 13

US-08-756-387B-13
 ; Sequence 13, Application US/08756387B
 ; Patent No. 5945294
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,387B
 FILING DATE: No. 5945294ember 26, 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: DI-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-756-387B-13

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RESULT 14

US-09-285-873-13
 ; Sequence 13, Application US/09285873
 ; Patent No. 6309832
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; APPLICANT: Porter, James P.
 ; APPLICANT: Rushlow, Keith E.
 ; APPLICANT: Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 ADDRESSEE: Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA: ..
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: verser, Carol talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-13

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Job time : 16.1422 secs

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Best Local Similarity 100.0%; Pred. No. 2.5e-84;
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RESULT 15
US-09-245-764-9
Sequence 9, Application US/09245764
Patent No. 6675105
GENERAL INFORMATION:
APPLICANT: Hogarth, P. Mark
APPLICANT: Powell, Maree S.
APPLICANT: McKenzie, Ian F.C.
APPLICANT: Maxwell, Kelly F.
APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vicana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
FILE REFERENCE: 4102-4
CURRENT APPLICATION NUMBER: US/09/245,764
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/099,994
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/073,972
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-245-764-9

Query Match 74.9%; Score 947; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.5e-84;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1264	100.0	257	9 US-09-944-277A-2	Sequence 2, Appli
3	1264	100.0	257	12 US-10-236-392-28	Sequence 28, Appli
4	1264	100.0	257	14 US-10-384-850-45	Sequence 45, Appli
5	1031.5	81.6	218	12 US-10-236-392-30	Sequence 30, Appli
6	969	76.7	176	10 US-09-809-715-2	Sequence 2, Appli
7	969	76.7	176	12 US-10-293-992-2	Sequence 2, Appli
8	947	74.9	172	9 US-09-944-277A-13	Sequence 13, Appli
9	947	74.9	172	9 US-09-245-764-9	Sequence 9, Appli
10	947	74.9	172	12 US-10-293-992-4	Sequence 4, Appli
11	947	74.9	172	12 US-10-687-109-9	Sequence 9, Appli
12	947	74.9	197	9 US-09-944-277A-11	Sequence 11, Appli
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14	785.5	62.1	236	15 US-10-434-817-7	Sequence 7, Appli
15	785.5	62.1	255	15 US-10-434-817-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-944-277A-6
; Sequence 6, Application US/09944277A
; Patent No. US30020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Ruslow, Keith E.
; Wassom, Donald E.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505

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US-10-027-736A-10
US-10-308-279-30
US-10-384-850-14
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US-10-106-698-5782
US-10-322-696-93
US-10-449-566-29
US-09-245-764-8
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US-10-027-736A-18
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US-10-384-850-43

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

Query Match          100.0%; Score 1264; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.3e-101; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

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DB 1 VPQPKVSLNPPWNRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 60
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
DB 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
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RESULT 2
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match          100.0%; Score 1264; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.7e-101; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

QY 1 VPQPKVSLNPPWNRIFKGENVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 60
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DB 86 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 145
QY 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
DB 206 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 257

RESULT 3
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Keskuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
```

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; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 28
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-236-392-28

Query Match      100.0%; Score 1264; DB 12; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.7e-101;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPNRRIFKGNVTLTCGNNFFVSVSTKWFHNGSLSEETNSSLIYNAKF 60
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCGNNFFVSVSTKWFHNGSLSEETNSSLIYNAKF 85

Qy 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145

Qy 121 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 146 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVILPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHPKNPKN 232
Db 206 FFIPLLVILPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHPKNPKN 257
```

RESULT 4

```
US-10-384-850-45
; Sequence 45, Application US/10384850
; Publication No. US20030175890A1
; GENERAL INFORMATION:
; APPLICANT: C. Fraser
; TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF
; FILE REFERENCE: 7853-217
; CURRENT APPLICATION NUMBER: US/10/384,850
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US/09/702,021
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-384-850-45

Query Match      100.0%; Score 1264; DB 14; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.7e-101;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPNRRIFKGNVTLTCGNNFFVSVSTKWFHNGSLSEETNSSLIYNAKF 60
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCGNNFFVSVSTKWFHNGSLSEETNSSLIYNAKF 85

Qy 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSEYKCOHQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
```

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Qy 121 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 146 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVILPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHPKNPKN 232
Db 206 FFIPLLVILPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHPKNPKN 257

RESULT 5
US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Laroche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shency, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenn
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 30
; LENGTH: 218
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-30

Query Match 81.6%; Score 1031.5; DB 12; Length 218;
Best Local Similarity 83.2%; Pred. No. 3.8e-81;
Matches 193; Conservative 0; Mismatches 0; Indels 39; Gaps 1;

QY 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 60
DB 26 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 85

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
DB 86 EDSEYK-----CHGWRNDVYKVIY 106

QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYLQ 180
DB 107 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYLQ 166

QY 181 FPIPLLVILFAVDGLSTQOQVTFLLKIKRTKGRFLLNPHKPNKN 232
DB 167 FPIPLLVILFAVDGLSTQOQVTFLLKIKRTKGRFLLNPHKPNKN 218

RESULT 6

US-09-809-715-2
; Sequence 2, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jardtzy, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-2

Query Match 76.7%; Score 969; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.5e-76;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 60
DB 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
DB 61 EDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176
DB 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176

RESULT 7

US-10-293-992-2
; Sequence 2, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jardtzy, Theodore S.

; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-2

Query Match 76.7%; Score 969; DB 12; Length 176;

Best Local Similarity 100.0%; Pred. No. 7.5e-76;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 60
DB 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNINAKF 60

QY 61 EDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120
DB 61 EDSEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176
DB 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176

RESULT 8

US-09-944-277A-13
; Sequence 13, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-944-277A-13

Query Match 74.9%; Score 947; DB 9; Length 172;
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 DB 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 QY 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 DB 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 9
 US-09-245-764-9
 ; Sequence 9, Application US/09245764
 ; Patent No. US20020107359A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hogarth, P. Mark
 ; APPLICANT: Powell, Maree S.
 ; APPLICANT: McKenzie, Ian F.C.
 ; APPLICANT: Maxwell, Kelly F.
 ; APPLICANT: Garrett, Thomas P.J.
 ; APPLICANT: Epa, Vidana
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
 ; FILE REFERENCE: 4102-4
 ; CURRENT APPLICATION NUMBER: US/09/245,764
 ; EARLIER FILING DATE: 1999-02-05
 ; EARLIER FILING DATE: 1998-09-11
 ; EARLIER FILING DATE: 1998-09-11
 ; EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-245-764-9

Query Match 74.9%; Score 947; DB 9; Length 172;
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 DB 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 QY 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 DB 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 10

US-10-293-992-4
 ; Sequence 4, Application US/10293992
 ; Publication No. US20040033527A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardetzky, Theodore S.
 ; APPLICANT: Garman, Scott Clayton
 ; APPLICANT: Kinet, Jean-Pierre
 ; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPTOR
 ; FILE REFERENCE: AL-3-C1-1
 ; CURRENT APPLICATION NUMBER: US/10/293,992
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 09/434,193
 ; PRIOR FILING DATE: 1999-11-04
 ; PRIOR APPLICATION NUMBER: 60/107,219
 ; PRIOR FILING DATE: 1998-11-05
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-293-992-4

Query Match 74.9%; Score 947; DB 12; Length 172;
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 DB 1 VPQKPKVSLNPWNRIFKGENVLTCTGNNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60
 QY 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 DB 61 EDSGEYKQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIY 120
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
 DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 11
 US-10-687-109-9
 ; Sequence 9, Application US/10687109
 ; Publication No. US20040054480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hogarth, P. Mark
 ; APPLICANT: Powell, Maree S.
 ; APPLICANT: McKenzie, Ian F.C.
 ; APPLICANT: Maxwell, Kelly F.
 ; APPLICANT: Garrett, Thomas P.J.
 ; APPLICANT: Epa, Vidana
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
 ; FILE REFERENCE: 4102-4
 ; CURRENT APPLICATION NUMBER: US/10/687,109
 ; CURRENT FILING DATE: 2003-10-15
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 172
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-687-109-9

Query Match 74.9%; Score 947; DB 12; Length 172;
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172
Db 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

RESULT 12

US-09-944-277A-11

; Sequence 11, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 197 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-944-277A-11

Query Match 74.9%; Score 947; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.9e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 85
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 120
Db 86 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 145

QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172
Db 146 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197

RESULT 13

US-09-809-715-4

; Sequence 4, Application US/09809715

; Publication No. US20030003052A1

; GENERAL INFORMATION:

; APPLICANT: Jaretzky, Theodore S.

; Garman, Scott Clayton

; APPLICANT: Warzburg, Beth A.

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC

; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN Ige

; FILE REFERENCE: AL-8

; CURRENT APPLICATION NUMBER: US/09/809,715

; CURRENT FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 60/189,853

; PRIOR FILING DATE: 2000-03-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 176

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-809-715-4

Query Match 74.7%; Score 944; DB 10; Length 176;
Best Local Similarity 97.7%; Pred. No. 1.1e-73;
Matches 172; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60
Db 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMWEGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKAPREK 176
Db 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKAPREK 176

RESULT 14

US-10-434-817-7

; Sequence 7, Application US/10434817

; Publication No. US20030235579A1

; GENERAL INFORMATION:

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA

; CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/434,817

; FILING DATE: 08-May-2003

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,734
FILING DATE: 29-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-434-817-7

Query Match 62.1%; Score 785.5; DB 15; Length 236;
Best Local Similarity 66.2%; Pred. No. 7.9e-60;
Matches 151; Conservative 29; Mismatches 43; Indels 5; Gaps 2;
QY 3 QKPKVSLNPPWNRIFKGENVLTCTGNNPFEVSTKWFHNGSLSEETNSSLNIVNAKPED 62
DB 9 RKTSTVSLNPPWNRIFKGENVLTCTGNNKPLKGNSTEWYNTTLEVTSSLNITNASHRS 68
QY 63 SGKYKCHQOVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGMRNDVYKVIYK 122
DB 69 SGYRCRNDNLSEAVHLEVFSDWLLLOASAEVIEGKALVLCRCGWKDWVFKVIYK 128
QY 123 DGEALKYWNHNISITNATVEDSGTYCTG----KWQLDYSEPLNITVIKAPREK-Y 177
DB 129 DGKPLEYWNKNISIESATENSSTYCEGAFNFKRTSERYTSDYLNITVKKAEQSKRY 188
QY 178 WLOFFIPLLVILFAVDTGIFSTQQQVTFLLKIKRTRKGRFLNPHP 225
DB 189 WLOFFIPLLVILFAVDTGIFSTQQQVTFLLKIKRTRRGRKLMDEHP 236

RESULT 15
US-10-434-817-2
Sequence 2, Application US/10434817
Publication No. US20030235579A1
GENERAL INFORMATION:
APPLICANT: Weber, Eric R.
McCall, Catherine A.
TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/434,817
FILING DATE: 08-May-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,734
FILING DATE: 29-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-434-817-2

Query Match 62.1%; Score 785.5; DB 15; Length 255;
Best Local Similarity 66.2%; Pred. No. 8.6e-60;
Matches 151; Conservative 29; Mismatches 43; Indels 5; Gaps 2;
QY 3 QKPKVSLNPPWNRIFKGENVLTCTGNNPFEVSTKWFHNGSLSEETNSSLNIVNAKPED 62
DB 28 RKTSTVSLNPPWNRIFKGENVLTCTGNNKPLKGNSTEWYNTTLEVTSSLNITNASHRS 87
QY 63 SGKYKCHQOVNESEPVYLEVFSWLLLOASAEVVMGQPLFLRCHGMRNDVYKVIYK 122
DB 88 SGYRCRNDNLSEAVHLEVFSDWLLLOASAEVIEGKALVLCRCGWKDWVFKVIYK 147
QY 123 DGEALKYWNHNISITNATVEDSGTYCTG----KWQLDYSEPLNITVIKAPREK-Y 177
DB 148 DGKPLEYWNKNISIESATENSSTYCEGAFNFKRTSERYTSDYLNITVKKAEQSKRY 207
QY 178 WLOFFIPLLVILFAVDTGIFSTQQQVTFLLKIKRTRKGRFLNPHP 225
DB 208 WLOFFIPLLVILFAVDTGIFSTQQQVTFLLKIKRTRRGRKLMDEHP 255

Search completed: October 6, 2004, 09:28:10
Job time : 71.8438 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 12.7086 Seconds
(without alignments)
1756.007 Million cell updates/sec

Title: US-10-763-400-6
Perfect score: 1264
Sequence: 1 VPQPKVSLNPPNRIKFGZ.....RTRKGFLLNPHKPNPKXN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1364	100.0	257	2	S00682
2	587.5	46.5	250	2	A34342
3	576.5	45.6	245	2	A30154
4	411.5	32.6	254	1	JU0107
5	399.5	31.6	233	1	JU0284
6	398.5	31.5	280	2	I55577
7	390	30.9	267	2	A35902
8	389	30.8	267	2	I36110
9	387.5	30.7	261	2	S29360
10	381	30.1	296	2	I46021
11	375	29.7	267	2	I72882
12	371.5	29.4	344	2	A41357
13	371.5	29.4	374	1	A39878
14	369	29.2	336	2	I48471
15	369	29.2	404	2	A46480
16	367	29.0	270	2	A34636
17	363.5	28.8	283	1	FCMS01
18	363.5	28.8	330	2	A40071
19	363.5	28.8	330	2	I49660
20	361.5	28.6	285	2	S36903
21	345	27.3	323	2	S06946
22	341	27.0	310	2	JU0119
23	338	26.9	160	2	I47163
24	338	26.9	317	2	JU0118
25	327	25.9	157	2	D31327
26	271	21.4	159	2	I47164
27	162.5	12.9	1694	2	S50065
28	148	11.7	104	2	I47165
29	137.5	10.9	458	1	WNMSR1

30 137.5 10.9 521 2 JC1508
31 136.5 10.8 458 2 JC1509
32 136.5 10.8 458 2 S23969
33 136.5 10.8 458 2 S68177
34 136.5 10.8 519 2 A44783
35 136.5 10.8 521 2 S34338
36 134 10.6 7962 2 JC2457
37 131 10.4 538 2 JC2457
38 129.5 10.2 344 2 A27681
39 129.5 10.2 1239 1 A32579
40 123 9.7 1033 2 S19247
41 122 9.7 1327 2 T09402
42 121 9.6 868 2 A46512
43 120.5 9.5 739 2 JS0675
44 120 9.5 647 2 A35648
45 120 9.5 862 2 I49583

ALIGNMENTS

RESULT 1

S00682

IGE FC receptor alpha chain precursor - human

N:Alternate names: FC-epsilon receptor

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: S00682; B30154; S42209

R:Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.

Nucleic Acids Res. 16, 3584, 1988

A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity

A:Reference number: S00682; MUID:88233953; PMID:2967464

A:Accession: S00682

A:Molecule type: mRNA

A:Residues: 1-257 <KOC>

A:Cross-references: EMBL:X05948; NID:g31317; PIDN:CAA30025.1; PID:g31318

R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988

A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization

A:Reference number: A34191; MUID:88158102; PMID:2964640

A:Accession: B30154

A:Molecule type: mRNA

A:Residues: 1-257 <SHI>

A:Cross-references: GB:J03605; NID:g187449; PIDN:AAA36204.1; PID:g307164

R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.

Eur. J. Biochem. 220, 593-598, 1994

A:Title: High-level expression of the truncated alpha chain of human high-affinity receptor

A:Reference number: S42209; MUID:94170811; PMID:8125119

A:Accession: S42209

A:Molecule type: protein

A:Residues: 26-197 <YAG>

A:Experimental source: purified recombinant protein

C:Genetics:

A:Gene: GDB:FCER1A

A:Cross-references: GDB:119902; OMIM:147140

A:Map position: 1q23-1q23

C:Superfamily: FC gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor; transmembrane protein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-257/Product: IGE FC receptor alpha chain #status predicted <KAT>

F:44-95/Domain: immunoglobulin homology <IMM1>

F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 1264; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 2.1e-92;

Mismatches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKFGZVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

Db 26 VPQPKVSLNPPNRIKFGZVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85

QY 61 EDSSEYKQCHQVNESEPVLYEVFSDWLLQLQAEVVMQCPFLRCHGRWHDVTKVIY 120

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Db      86  DSGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVMEGQPLFURCHGWRNDVYKVIY 145
QY      121  YKDGALKYWNHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKAPREKYWLQ 180
Db      146  YKDGALKYWNHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKAPREKYWLQ 205
QY      181  FFIPLLVILFAVDLGLFSTCOQVTFLLKIKRFGRLNPHKPNKPN 232
Db      206  FFIPLLVILFAVDLGLFSTCOQVTFLLKIKRFGRLNPHKPNKPN 257

RESULT 2
A34342
A:Species: Mus musculus (house mouse)
A:Title: Ige receptor alpha chain precursor - mouse
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
C:Accession: A34342; A61238
R:Ra, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A:Title: Complete structure of the mouse mast cell receptor for Ige (Fc-epsilon-RI) and
A:Reference number: A34342; MUID:89359361; PMID:2527850
A:Accession: A34342
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-250 <RA>
A:Cross-references: GB:J05018; NID:G193236; PIDN:AAA37600.1; PID:G309224
R:Robertson, M.W.; Mehl, V.S.; Richards, M.L.; Liu, F.T.
Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991
A:Title: mRNA variants encoding multiple forms of the high-affinity Ige receptor alpha s
A:Reference number: A61238; MUID:92234569; PMID:1839735
A:Accession: A61238
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 125-194 <RB>
A:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:42-94/Domain: immunoglobulin homology <IMM>

Query Match 46.5%; Score 587.5; DB 2; Length 250;
Best Local Similarity 52.3%; Pred. No. 4e-39;
Matches 113; Conservative 43; Mismatches 57; Indels 3; Gaps 3;

QY      3  QKPKVSLNPPNRIKGENVILTCGNPFPEV-SSTKWFNGSLSEETNSLNIIVNAKFE 61
Db      26  EKSVLTLDPPIRIFTGEKVTLSYGNHQLQMSSTTKWIHNGTIVSEVNSHLVIVSATVQ 85
QY      62  DSGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVMEGQPLFURCHGWRNDVYKVIY 121
Db      86  DSGYIKCOQGLFKSPVILNTQDWLLQTSADMLLVHGSFDIRCHGWRNDVYKVIY 145
QY      122  KDGALKYWNHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKAPREK-YWLQ 180
Db      146  RNDHAFNYSYBS-PVSIREATLNDSTGYHCKGYLRQVEYSDKFRFIAVVKAYKCKYWLQ 204
QY      181  FFIPLLVILFAVDLGLFSTCOQVTFLLKIKRTRK 216
Db      205  LIFFLVAILFAVDLGLLSTEEQFKSVLEIQKTRG 240

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RESULT 3

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A30154
A:Species: Ige receptor alpha chain precursor - rat
N:Alternate names: Fc-epsilon-R alpha chain precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
C:Accession: C31327; A31327; A30154; A27116; I55304
R:Liu, P.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ige
A:Reference number: A94203; MUID:88289772; PMID:2969594
A:Accession: C31327
A:Molecule type: mRNA

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RESULT 4

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JL0107
Fc gamma (IgG) receptor III-A precursor (natural killer cell) [validated] - human
N:Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surf
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 08-Dec-2000
C:Accession: JL0107; A60383; A32933; I37627
R:Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A:Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A:Reference number: JL0107; MUID:89328325; PMID:2526846
A:Accession: JL0107
A:Molecule type: mRNA
A:Residues: 1-254 <RAV>

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A:Residues: 1-245 <LIU>
A:Cross-references: GB:M21622; GB:J03811
A:Experimental source: basophilic leukemia cell line, clone R3-4
A:Accession: A31327
A:Molecule type: mRNA
A:Residues: 21-245 <LI>
A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811
A:Experimental source: basophilic leukemia cell line
R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterized
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: A30154
A:Molecule type: mRNA
A:Residues: 1-245 <SHI>
A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332
R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff
A:Reference number: A27116; MUID:88024987; PMID:2959318
A:Accession: A27116
A:Molecule type: mRNA
A:Residues: 1-'G', 3-236, 'N', 238-244, 'RLKPNS' <KIN>
R:Tepler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A:Title: The gene for the rat mast cell high affinity Ige receptor alpha chain. Structur
A:Reference number: I55304; MUID:89174653; PMID:2522441
A:Accession: I53304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:44-245/Product: Ige receptor alpha chain #status predicted <MAT>
F:42-93/Domain: immunoglobulin homology <IMM>

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Query Match 45.6%; Score 576.5; DB 2; Length 245;

Best Local Similarity 51.4%; Pred. No. 2.9e-38;

Matches 111; Conservative 39; Mismatches 65; Indels 1; Gaps 1;

QY 3 QKPKVSLNPPNRIKGENVILTCGNPFPEV-SSTKWFNGSLSEETNSLNIIVNAKFE 62

Db 26 QKSVVSLDPPPIRIITGDKVTLCGNNSQMSSTKWIHNDISNKKSHWIVSATIQD 85

QY 63 SGEYKCOHQVNESEPVYLEVFSDFWLLQASAEVMEGQPLFURCHGWRNDVYKVIY 122

Db 86 SGEYIKCOQGLFKSPVILNTQDWLLQTSADMLLVHGSFDIRCHGWRNDVYKVIY 145

QY 123 DGEALKYWNHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKAPREK-YWLQ 181

Db 146 DDIAFKSYSDSNISIRKATFNDSGYHCTGYLNKVECKSKFSAIVVVKDYTYEYRWLQ 205

QY 182 FIPLLVILFAVDLGLFSTCOQVTFLLKIKRTRK 217

Db 206 IFPSLAVILFAVDLGLFWFTHKQFESILKIKTRK 241

C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 28-Jan-2000
C;Accession: J00284; S00758; I37628; B32933; A31460
R;Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: J0107; MUID:89328325; PMID:2526846
A;Accession: J00284
A;Molecule type: mRNA
A;Residues: 1-201,'SF',204-233 <RAV>
A;Cross-references: GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, d1
rSimmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane
A;Reference number: S00758; MUID:88232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA
A;Residues: 1-233 <SIM>
A;Cross-references: EMBL:X07934; NID:929744; PIDN:CAA30758.1; PID:G29745
R;Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:9559446; PIDN:CAA86296.1; PID:G871306
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
C;Comment: This low affinity IgG Fc receptor of natural killer cells, which is the produ
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in
C;Genetics:
A;Gene: GDB:FCGR3A; FCGR3
A;Cross-references: GDB:I119904; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: Glycoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-254/Product: Fc gamma (IgG) receptor III-A #status experimental <MAT>
F;18-208/Domain: extracellular #status predicted <EXT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;209-229/Domain: transmembrane #status predicted <TR>
F;230-254/Domain: intracellular #status predicted <CY>
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 32.6%; Score 411.5; DB 1; Length 254;
Best Local Similarity 41.6%; Pred. No. 3e-25;
Matches 87; Conservative 33; Mismatches 82; Indels 7; Gaps 1;
QY 4 KPKVSLNPPNRIKGNVTLTCGNFFVSTKTFHNGSLSEETNSLNIVNAKFEDS 63
DB 25 KAVVLEPQWYVLEKDSVTLKCGAYSPEDNSTOWFHNSLSSQASSYFIDAATVDDS 84
QY 64 GEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLFLRCHGWNDVVKVYYKD 123
DB 85 GEYRCOTNLSTLSDPQVLEHIGWLLQAPRWFKEDPFLRCHGWNDVVKVYYKD 144
QY 124 GEALKYWEHNIISITNATVEDSTGYCTGKWLQDYSEPLNITVTKAPREKYLQFFI 183
DB 145 GKGRKYFHNSDFVPRATLKDSGYFCRGLFGSKNVSSTVNTITQGLAVSTISSFFP 204
QY 184 P-----LLVVLFAVDTGFLFSTQQOV 205
DB 205 PGYQVSCFLVMLLFAVDTGFLFSVKNTNI 233
RESULT 5
J00284
Fc gamma (IgG) receptor III-B precursor (neutrophil) - human
N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra
C;Species: Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 28-Jan-2000
C;Accession: J00284; S00758; I37628; B32933; A31460
R;Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: J0107; MUID:89328325; PMID:2526846
A;Accession: J00284
A;Molecule type: mRNA
A;Residues: 1-201,'SF',204-233 <RAV>
A;Cross-references: GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, d1
rSimmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane
A;Reference number: S00758; MUID:88232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA
A;Residues: 1-233 <SIM>
A;Cross-references: EMBL:X07934; NID:929744; PIDN:CAA30758.1; PID:G29745
R;Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:9559446; PIDN:CAA86296.1; PID:G871306
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
C;Comment: This low affinity IgG Fc receptor exists in both polypeptide-anchored and phosph
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: B32933
A;Molecule type: mRNA
A;Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A;Cross-references: GB:M24854; NID:9184851; PIDN:AAA53507.1; PID:G306930
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A;Reference number: A31460; MUID:89128838; PMID:2521732
A;Accession: A31460
A;Molecule type: mRNA
A;Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A;Cross-references: GB:J04162; NID:9183036; PIDN:AAA35881.1; PID:G183037
C;Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the
1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
C;Genetics:
A;Gene: GDB:FCGR3B; FCGR3
A;Cross-references: GDB:I28176; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;56,63,92,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
Query Match 31.6%; Score 399.5; DB 1; Length 233;
Best Local Similarity 41.1%; Pred. No. 2.4e-24;
Matches 86; Conservative 32; Mismatches 84; Indels 7; Gaps 1;
QY 4 KPKVSLNPPNRIKGNVTLTCGNFFVSTKTFHNGSLSEETNSLNIVNAKFEDS 63
DB 25 KAVVLEPQWYVLEKDSVTLKCGAYSPEDNSTOWFHNSLSSQASSYFIDAATVDDS 84
QY 64 GEYKCOHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLFLRCHGWNDVVKVYYKD 123
DB 85 GEYRCOTNLSTLSDPQVLEHIGWLLQAPRWFKEDPFLRCHGWNDVVKVYYKD 144

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S29360; S46999
R;Ravetch, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H
Science 234, 718-725, 1986
A;Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc
A;Reference number: S29360; MUID:87042761; PMID:2946078
A;Accession: S29360
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <RAV>
A;Cross-references: EMBL:M14215; NID:G193247; PIDN:AAA37604.1; PID:G309228
R;Feinman, R.; Qiu, W.Q.; Pearse, R.N.; Nikolaiczky, B.S.; Sen, R.; Sheffery, M.; Raveto
EMBO J. 13, 3852-3860, 1994
A;Title: PU.1 and an HLH family member contribute to the myeloid-specific transcription
A;Reference number: S46999; MUID:94349933; PMID:8070412
A;Accession: S46999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <FEI>
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;130-183/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 387.5; DB 2; Length 261;
Best Local Similarity 35.7%; Pred. No. 2.4e-23;
Matches 84; Conservative 43; Mismatches 93; Indels 15; Gaps 5;

QY 4 KPKVSLNPPNRIKGENVTLTCNGNNFEVSTKWFHNG-SLSEETNSLSLIVNAKFD 62
DB 34 KAVKLDPPMIQVLKEDVILMEGTHNPGNSSTQWFHNGRSRSQVQASYTF-KATVND 92

QY 63 SGEYKQHQVNESEPVYLEVFDLWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122
DB 93 SGEYRCQMEQTRLSDPVDLQVSDWLLQTPQRFLEGETITLRCHSWRNKLNRISEFF 152

QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKWLQDYSEPLNITV---IKAPREKYW 178
DB 153 NERSVRYHYKNSFIPKANSHSGDYCKGSLGSGTQHQSKPVTITVQDPATTSSISLVW 212

QY 179 LQFFIPILLVILFAVDTLGLFISTQVTFLLKIKTRKGRF---LLNPHKPNK 230
DB 213 YHTAFSLVMCLLFAVDTLGLFYVRR-----NLQTPREYKWSLSIRKHQAPQDK 261

RESULT 10
I46021
Fc-gamma receptor II - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
C;Accession: I46021; S40204
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
A;Reference number: I46021; MUID:94245284; PMID:8188320
A;Accession: I46021
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-296 <ZHA>
A;Cross-references: EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G437979
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor

Query Match 30.1%; Score 381; DB 2; Length 296;
Best Local Similarity 41.2%; Pred. No. 9.1e-23;
Matches 70; Conservative 33; Mismatches 65; Indels 1;

QY 2 POKPK--VSLNPPNRIKGENVTLTCNGNNFEVSTKWFHNGSLSEETNSLSLIVNAK 59
DB 44 PDLKAVVTIQPANVILREHVTILTCGTSTFSAGNLTTFHNGSSITHTQPSYSFRAG 103

QY 60 FEDSGEYKQHQVNESEPVYLEVFDLWLLQASAEVVMGQPLFLRCHGWRNWDVYKVI 119
DB 104 SNDSGSVRCQREQTSLSDPVLQVSDWLLQTPSLVFQEGEIMLRCHSWRNQPLNKIT 163

QY 120 YKDGKALKWYENHNISITNATVEDSGTYCTGKWLQDYSEPLNITV 169
DB 164 FYQDKSKIFSYQRTNFIPIRANLSHSGYHCTAFIGKMLHSSQPVNITV 213

RESULT 11
I72882
Fc gamma receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I72882
R;Sears, D.
J. Immunol. 150, 4364-4375, 1993
A;Title: Rat Class III Fc gamma receptor isoforms differ in IgG subclass-binding speci
A;Reference number: I56166; MUID:93246650; PMID:8482840
A;Accession: I72882
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: GB:L08446; NID:G204120; PIDN:AAA41151.1; PID:G204121
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;55-106/Domain: immunoglobulin homology <IMM>

Query Match 29.7%; Score 375; DB 2; Length 267;
Best Local Similarity 36.9%; Pred. No. 2.4e-22;
Matches 76; Conservative 42; Mismatches 84; Indels 4; Gaps 1;

QY 4 KPKVSLNPPNRIKGENVTLTCNGNNFEVSTKWFHNGSLSEETNSLSLIVNAKFD 63
DB 40 KAVKLDPPMIQVLKDDVTLTCGTHNPGNSSTQWFHNGRSRSQVQASYTFKATVND 99

QY 64 SGEYKQHQVNESEPVYLEVFDLWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 123
DB 100 SGEYRCMAFTSLSDPVLQVSDWLLQTPQRFLEGERITLRCHGWKSIQLARISFLQ 159

QY 124 DGEALKWYENHNISITNATVEDSGTYCTGKWLQDYSEPLNITV---IKAPREKYW 179
DB 160 GFVFSFHPYVNSYSLSNANSHSGDYCKAYLGRTEHVSKVTTITVQGSATATSSSLVWF 219

QY 180 QFFIPLVILFAVDTLGLFISTQVTFLLKIKTRKGRF---LLNPHKPNK 205
DB 220 HAAFLVLMCLLFAVDTLGLFYVRR-----NLQTPREYKWSLSIRKHQAPQDK 245

RESULT 12
A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jan-2000
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL>
A;Cross-references: GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; PID:G31334
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL>
A;Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A;Note: the authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 29.4%; Score 371.5; DB 2; Length 344;
 Best Local Similarity 41.0%; Pred. No. 6e-22;
 Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWRIKFGENVTLTCNGNFFVSSSTKWFHNGSLSEBTSSLNIVNAKPEDS 63
 DB 21 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQTSYRITSASVND 80
 QY 64 GEYKCOHQVNESEPVYLEVFSMDLLQASAEVVMGQPLFLRCHGWRNMDVYKVIYKD 123
 DB 81 GEYRCQGLSGRSDPIQLIEHSGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 140

QY 124 GEALKYWHYENHISITNATVDSGYCTGKWQLDYSEPLNITV 169
 DB 141 GKAFKFFHWSNLTKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 13

A39878
 Fc gamma (IgG) receptor I-A (high affinity) precursor - human
 N:Alternate names: CD64
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence revision 06-Sep-1996 #text_change 21-Jul-2000
 C:Accession: A39878; I70304; B41357; S03018; I57525
 R:van de Winkel, J.G.J.; Ernst, L.K.; Anderson, C.L.; Chiu, I.M.
 J. Biol. Chem. 266, 13449-13455, 1991
 A:Title: Gene organization of the human high affinity receptor for IgG, Fc gammaRI (CD64)
 A:Reference number: A39878; MUID:91302383; PMID:1830050
 A:Accession: A39878
 A:Molecule type: DNA
 A:Residues: 1-374 <V>
 A:Cross-references: GB:M63830; GB:M63835; NID:g180277; PIDN:AAA35678.1; PID:g180279
 R:Porces, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.
 J. Clin. Invest. 90, 2102-2109, 1992
 A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
 A:Reference number: I55577; MUID:93055454; PMID:1430234
 A:Accession: I70304
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-374 <RES>
 A:Cross-references: GB:L03418; NID:g184840; PIDN:AAA36049.1; PID:g292169
 R:Allen, J.M.; Seed, B.
 Science 243, 378-381, 1989
 A:Title: Isolation and expression of functional high-affinity Fc receptor complementary
 A:Reference number: A41357; MUID:89100284; PMID:2911749
 A:Accession: B41357
 A:Molecule type: mRNA
 A:Residues: 1-24, 'S', '26-337', 'T', '339-374' <AL1>
 A:Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332
 R:Allen, J.M.; Seed, B.
 Nucleic Acids Res. 16, 11824, 1988
 A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR
 A:Reference number: S03018; MUID:89098339; PMID:2974947
 A:Accession: S03018
 A:Molecule type: mRNA
 A:Residues: 1-24, 'S', '26-337', 'T', '339-374' <AL2>
 A:Cross-references: GB:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332
 R:Perez, C.; Wietzerbin, J.; Benech, P.D.
 Mol. Cell. Biol. 13, 2182-2192, 1993
 A:Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma int
 A:Reference number: I57525; MUID:93204964; PMID:8455606
 A:Accession: I57525
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <RE2>
 A:Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587
 C:Genetics:
 A:Gene: GDB:FCGRIA; CD64
 A:Cross-references: GDB:I35911; OMIM:146760
 A:Map position: 1q21-1q21
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology

C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-292/Domain: extracellular #status predicted <EXT>
 F:117-170/Domain: immunoglobulin homology <IMM2>
 F:293-313/Domain: transmembrane #status predicted <TM>
 F:59,78,152,159,163,195,240/Binding site: carboxydrate (Asn) (covalent) #status predi

Query Match 29.4%; Score 371.5; DB 1; Length 374;
 Best Local Similarity 41.0%; Pred. No. 6.e-22;
 Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWRIKFGENVTLTCNGNFFVSSSTKWFHNGSLSEBTSSLNIVNAKPEDS 63
 DB 21 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQTSYRITSASVND 80
 QY 64 GEYKCOHQVNESEPVYLEVFSMDLLQASAEVVMGQPLFLRCHGWRNMDVYKVIYKD 123
 DB 81 GEYRCQGLSGRSDPIQLIEHSGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 140

QY 124 GEALKYWHYENHISITNATVDSGYCTGKWQLDYSEPLNITV 169
 DB 141 GKAFKFFHWSNLTKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 14

I48471
 Fc gamma (IgG) receptor high affinity - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 21-Jan-2000
 C:Accession: I48471
 R:Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
 Science 260, 695-698, 1993
 A:Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
 A:Reference number: I48471; MUID:93242399; PMID:8480181
 A:Accession: I48471
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-336 <RES>
 A:Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology
 C:Keywords: immunoglobulin receptor
 F:128-180/Domain: immunoglobulin homology <IMM>

Query Match 29.2%; Score 369; DB 2; Length 336;
 Best Local Similarity 38.8%; Pred. No. 9.2e-22;
 Matches 85; Conservative 40; Mismatches 82; Indels 12; Gaps 6;

QY 4 KPKVSLNPPWRIKFGENVTLTCNGNFFVSSSTKWFHNGSLSEBTSSLNIVNAKPEDS 63
 DB 31 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQTSYRITSASVND 90
 QY 64 GEYKCOHQVNESEPVYLEVFSMDLLQASAEVVMGQPLFLRCHGWRNMDVYKVIYKD 122
 DB 91 GEYRCQGLSGRSDPIQLIEHSGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 150

QY 123 DEALKYWHYENHISITNATVDSGYCTGKWQLDYSEPLNITV KAPREKXWQFF 182
 DB 151 NGKSPKF-SGSKTALKTNLSHGSIHVCSSG-MGRHRYTSAGISITVKAFFLE---LFT 204
 QY 183 IPLL-VVILFAVDVGLFSTQQQVTFLLKIKRTRKGPRL 220
 DB 205 TPVLRASVSPFPGSLVLTNCEINLLQ-----RPGQLQ 239

RESULT 15

A46480
 Fc gamma (IgG) receptor high affinity - mouse
 N:Alternate names: high affinity IgG receptor
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A46480; A43511
 R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
 J. Immunol. 148, 1570-1575, 1992

A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A;Reference number: A46480; MUID:92166399; PMID:1531670
A;Accession: A46480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <OSM>
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A;Reference number: A43511; MUID:90111035; PMID:2136886
A;Accession: A43511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <SEA>
A;Cross-references: GB:M31314; NID:G200752; PIDN:AAA40056.1; PID:G200753
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 29.2%; Score 369; DB 2; Length 404;
Best Local Similarity 43.4%; Pred. No. 1.le-21;
Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;

Qy 4 KPVSINPPNRIKGENVLTCTGNKFFVSVSTKWFHNGSLSEETNSSLINIVNAKFDS 63
Db 31 KAVITLQPPWVSIFQENVTWCCEGPHLPCDSDSIQNFINGTAVQISTPYSIPEASFQDS 90
Qy 64 GEYKCOHQVNESEPVYLEVFSDFMLLQASAEVYMEGQPLFLRCHGRNNDVYKVIYKD 123
Db 91 GEYRCQIGSSMPSPVQLQIHNDWLLQLQASRRVLTEGEPLALRCHGKKNKLVYVYFYN 150
Qy 124 GEALKYWEHNISITNATVEDSGYYCTGKWQLDYSEPLNITY 169
Db 151 GKSFQF-SSDSEVAILKTNLSHSGIYHCSG-TGRHRYTSAGVSITY 194

Search completed: October 6, 2004, 09:23:42
Job time : 13.7086 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 7.84149 Seconds
(without alignments)
1540.558 Million cell updates/sec

Title: US-10-763-400-6

Perfect score: 1264

Sequence: 1 VPQKPKVSLNPPMNRIFKGE.....RTRKGFRLNPPKPNPKN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1264	100.0	257	1 FCEA HUMAN	P12319 homo sapien
2	597.5	46.5	250	1 FCEA MOUSE	P20489 mus musculus
3	576.5	45.6	245	1 FCE1 RAT	P12371 rattus norv
4	413.5	32.7	250	1 FCG3 BOVIN	P79107 bos taurus
5	411.5	32.6	254	1 FC3A HUMAN	P08637 homo sapien
6	411	32.5	257	1 FCG3_PIG	Q28942 sus scrofa
7	399.5	31.6	233	1 FC3B HUMAN	P075015 homo sapien
8	390	30.9	267	1 FCG3 RAT	P27645 rattus norv
9	387.5	30.7	261	1 FCG3 MOUSE	P08508 mus musculus
10	381	30.1	296	1 FCG2 BOVIN	Q28110 bos taurus
11	374.5	29.6	374	1 FCG1 HUMAN	P12314 homo sapien
12	370.5	29.3	341	1 FCG3_CAVPO	Q60513 cavia porce
13	369	29.2	404	1 FCG1_MOUSE	P26151 mus musculus
14	363.5	28.8	330	1 FCG2_MOUSE	P08101 mus musculus
15	361.5	28.6	285	1 FCG2 RAT	Q63203 rattus norv
16	345	27.3	310	1 FCGB HUMAN	P31994 homo sapien
17	345	27.3	323	1 FCGC HUMAN	P31995 homo sapien
18	341.5	27.0	316	1 FCGA_PANTR	Q85978 pan troglod
19	328	25.9	317	1 FCG3_HUMAN	P12318 homo sapien
20	327	25.9	157	1 FCE2 RAT	P12840 rattus norv
21	170	13.4	1709	1 SN HUMAN	Q9b222 homo sapien
22	162.5	12.9	1694	1 SN_MOUSE	Q62230 mus musculus
23	154	12.2	422	1 K3L1 RAT	P83556 rattus norv
24	144	11.4	432	1 K3L1_MOUSE	P83555 mus musculus
25	137.5	10.9	521	1 CEAL_MOUSE	P31809 mus musculus
26	136.5	10.8	519	1 ECTO_RAT	P16573 rattus norv
27	136	10.8	837	1 NCM2_MOUSE	Q35136 mus musculus
28	129.5	10.2	1302	1 NRG_DROME	P20241 drosophila
29	128.5	10.2	344	1 CEAG_HUMAN	P40199 homo sapien
30	126	10.0	1240	1 NFAS_HUMAN	Q94856 homo sapien
31	123	9.7	1240	1 NFAS_MOUSE	Q810u3 mus musculus
32	123	9.7	1240	1 NFAS_RAT	P97685 rattus norv
33	120.5	9.5	739	1 VCA1_RAT	P29534 rattus norv

ALIGNMENTS

RESULT 1

FCEA_HUMAN

ID FCEA_HUMAN STANDARD; PRT; 257 AA.

AC P12319;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor

DE (FCER1) (IGE Fc receptor, alpha-subunit) (FC-epsilon RI-alpha).

GN FCER1A OR FCER1A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=89233953; PubMed=2967464;

RA Kocchan J., Pettine L.F., Hakimi J., Kishi X., Kinet J.-P.;

RT "Isolation of the gene coding for the alpha subunit of the human high

RT affinity IGE receptor."

RL Nucleic Acids Res. 16:3584-3584(1988).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Mast cells;

RX MEDLINE=89158102; PubMed=2964640;

RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,

RA Leder P.;

RT "Human and rat mast cell high-affinity immunoglobulin E receptors:

RT characterization of putative alpha-chain gene products.";

Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).

RN [3]

RP 3D-STRUCTURE MODELING OF 26-137.

RX MEDLINE=931113350; PubMed=1472946;

RA Padlan E.A., Helm B.A.;

RT "A modeling study of the alpha-subunit of human high-affinity

RT receptor for immunoglobulin-E.";

Proc. Natl. Acad. Sci. U.S.A. 89:1129-1134(1992).

CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH

CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC

CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL

CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)

CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR

CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.

CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO

CC DISULFIDE LINKED GAMMA CHAINS.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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CC

DR EMBL; X06948; CAA30025.1; -;
 DR EMBL; J03605; AAA36204.1; -;
 DR EMBL; A21606; CAA01564.1; -;
 DR PIR; S00682; S00682.
 DR PDB; 1ALS; 27-FEB-95.
 DR PDB; 1ALT; 27-FEB-95.
 DR PDB; 1F2Q; 08-JUN-00.
 DR PDB; 1J86; 29-AUG-01.
 DR PDB; 1J87; 29-AUG-01.
 DR PDB; 1J88; 29-AUG-01.
 DR PDB; 1J89; 05-SEP-01.
 DR Genew; HGNC:3609; FCER1A.
 DR MIM; 147140; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00408; Igc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 257
 FT HIGH AFFINITY IMMUNOGLOBULIN EPSILON
 FT RECEPTOR ALPHA-SUBUNIT.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE 1.
 FT IG-LIKE 2.
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 46 46
 FT CARBOHYD 67 67
 FT CARBOHYD 75 75
 FT CARBOHYD 99 99
 FT CARBOHYD 160 160
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT STRAND 31 35
 FT HELIX 39 43
 FT TURN 43 43
 FT STRAND 48 54
 FT STRAND 61 66
 FT TURN 67 68
 FT STRAND 69 71
 FT STRAND 74 74
 FT TURN 75 76
 FT STRAND 77 79
 FT HELIX 82 87
 FT STRAND 91 96
 FT STRAND 98 100
 FT TURN 101 101
 FT STRAND 104 107
 FT STRAND 114 116
 FT HELIX 120 124
 FT STRAND 128 133
 FT STRAND 143 145
 FT HELIX 146 148
 FT TURN 149 149
 FT STRAND 150 150
 FT TURN 152 153
 FT STRAND 154 155
 FT TURN 156 159
 FT STRAND 160 163
 FT HELIX 165 170
 FT STRAND 175 178
 FT STRAND 181 182
 FT TURN 183 185
 FT STRAND 186 187
 FT STRAND 190 193
 SQ SEQUENCE 257 AA; 29596 MW; F183B2357DDAD58 CRC64;
 Query Match 100.0%; Score 1264; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 6.3e-99;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VFQKPKVSLNPPWNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLAINAKF 60
 DB 26 VFQKPKVSLNPPWNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLAINAKF 85
 QY 61 EDSEYKCHQHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNWDYKVIY 120
 DB 86 EDSEYKCHQHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNWDYKVIY 145
 QY 121 YKDGALKYVYENHNISITNATVDSGYCTGKVMQDYESEPLNIVIKAPREKYWLQ 180
 DB 146 YKDGALKYVYENHNISITNATVDSGYCTGKVMQDYESEPLNIVIKAPREKYWLQ 205
 QY 181 FFIPLVILFAVDTGFLFISTQQQVTFLLKIKRTRKGRFLNPPKPKNN 232
 DB 206 FFIPLVILFAVDTGFLFISTQQQVTFLLKIKRTRKGRFLNPPKPKNN 257
 RESULT 2
 FCEA MOUSE
 ID FCEA MOUSE STANDARD; PRT; 250 AA.
 AC P20489;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
 GN FCER1A OR FCE1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359361; PubMed=2527850;
 RA Ra C., Jouvin M.H.E., Kinet J.-P.;
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc epsilon RI) and surface expression of chimeric receptors (rat-mouse-human) on transfected cells.";
 RL J. Biol. Chem. 264:15323-15327(1989).
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE) RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMMA CHAINS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
 CC -----
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 CC -----
 CC EMBL; J05018; AAA37600.1; -;
 DR PIR; A34342; A34342.
 DR HSSP; P12319; 1ALS.
 DR MGD; MGI:95494; Fcer1a.
 DR GO; GO:0007165; P:signal transduction; IDA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003599; IG.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.

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FT SIGNAL 1 23 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT CHAIN 24 250 RECEPTOR ALPHA-SUBUNIT.
FT DOMAIN 24 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 250 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 104 IG-LIKE 1.
FT DOMAIN 114 181 IG-LIKE 2.
FT DISULFID 49 92 BY SIMILARITY.
FT DISULFID 131 174 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BFB4DC0C4E CRC64;

Query Match 46.5%; Score 587.5; DB 1; Length 250;
Best Local Similarity 52.3%; Pred. No. 3e-42;
Matches 113; Conservative 43; Mismatches 57; Indels 3; Gaps 3;

QY 3 QKPKVSLNPPNRIKGENVTLCNGNPFV-SSTKWFHNGSLSEETSSLNINVAKE 61
DB 26 EKVLTLDPEWIRIFTGEKVTLSCYGNHLMQNSTTKWIHNGTVSEVNSHLIVSATVQ 85

QY 62 DSSEYKCOHQVNESEPVYLEVFSDFMLLOASAEVMEGQPLFLRCHGWRNWDVYKVIY 121
DB 86 DSKYICQKQGLPKSPKPVYLVNTQDMLLQTSADMILVHGSFDIRCHGKNWVRKVIY 145

QY 122 KDGEALKYWHNNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREK-YWLO 180
DB 146 RNDHAFNYSVES-PVSIREATLNSGTYHCKGYLRQVEYSDKFRVAVKAYKCKYWLQ 204

QY 181 FTFPLLVILFAVDTGIFSTQGVTFLLKIKSTRK 216
DB 205 LIFPLLVAILFAVDTGILLSTEQKSVLEIQTKG 240

RESULT 3
FCEI_RAT STANDARD; PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (PCR1) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
DE GN FCB1A OR FCB1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakimi J., Kochan J.;
RA "A cDNA presumptively coding for the alpha subunit of the receptor
RT with high affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RN [2]
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE= Mast cells;
RX MEDLINE=88158102; PubMed=2264640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).

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RN [4]
RP SEQUENCE OF 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;
RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity Ige receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC !- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LIPIDOKINES.
CC !- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC !- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC !- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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CC
CC EMBL; M17153; AAA42045.1; -
CC EMBL; J03606; AAA41582.1; -
CC EMBL; M21622; AAA41146.1; -
CC PIR; C31327; A30154.
CC HSP; F12319; 1AUS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC Pfam; PF00047; IG; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS50835; IG LIKE; 1.
KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 245 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT DOMAIN 24 204 RECEPTOR ALPHA-SUBUNIT.
FT TRANSMEM 205 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 224 245 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 103 IG-LIKE 1.
FT DOMAIN 113 181 IG-LIKE 2.
FT DISULFID 49 91 BY SIMILARITY.
FT DISULFID 130 174 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 245 AA; 27793 MW; A0B67DD363B72197 CRC64;

Query Match 45.6%; Score 576.5; DB 1; Length 245;
Best Local Similarity 51.4%; Pred. No. 2.5e-41;
Matches 111; Conservative 39; Mismatches 65; Indels 1; Gaps 1;

QY 3 QKPKVSLNPPNRIKGENVTLCNGNPFV-SSTKWFHNGSLSEETSSLNINVAKE 62
DB 26 QKSVSLDPPWIRILTDGKVTLCNGNNSQMNKWIHNDISINVKSHHWIVSATIQD 85

QY 63 SGEYKCOHQVNESEPVYLEVFSDFMLLOASAEVMEGQPLFLRCHGWRNWDVYKVIY 122
DB 86 SGKYICQKQGLPKSPKPVYLVNTQDMLLQTSADMILVHGSFDIRCHGKNWVRKVIY 145

QY 123 DGEALKYWHNNHISITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPREK-YWLO 181
DB 146 DDAFKYSDSNISIRKATFNDSSGSHCTGYLNKVECKSDFSAVAVKDYTIETVWLQ 205

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QY 182 FPLLLVILFAVDLTGLFISTQQQVTFLLKIKETKRG 217
 DB 206 IFPSLAVILFAVDLTGLFWSTHFKQFESILKIKETKRG 241

RESULT 4
 FC3A_HUMAN STANDARD; PRT; 250 AA.
 AC P79107;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region precursor
 DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).
 GN FCGR3 OR FCGR3L.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node;
 RX MEDLINE=97246739; PubMed=9089104;
 RA Collins R.A., Gelder K.I., Howard C.J.;
 RT "Nucleotide sequence of cattle FCGR3L: its identification in
 RT gamma/delta T cells.";
 RL Immunogenetics 45:440-443(1997).
 CC !- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED
 CC OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTI-BODY-
 CC DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).
 CC !- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC !- SIMILARITY: EXPRESSED IN GAMMA-DELTA T CELLS.
 CC !- TISSUE SPECIFICITY: Contains 2 immunoglobulin-like C2-type domains.
 CC !- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT
 CC ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.
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EMBL; X99695; CAA68026.1; -;
 HSSP; P12319; IALS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 2.
 DR PROSITE; PS50835; IG LIKE; 2.
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1 16
 FT CHAIN 17 250
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT REGION RECEPTOR III.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 225
 FT DOMAIN 209 225
 FT DOMAIN 226 250
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 23 105
 FT DOMAIN 99 189
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT BY SIMILARITY.
 FT DISULFID 47 89
 FT BY SIMILARITY.
 FT DISULFID 128 172
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 63 63
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 180 180
 FT P -> L.
 FT VARIANT 11 11
 FT VARIANT 12 12
 FT VARIANT 46 46
 FT VARIANT 107 107
 FT VARIANT 114 114
 FT VARIANT 114 114
 FT VARIANT 229 229
 FT V -> I.
 SQ SEQUENCE 250 AA; 28050 MW; DE625139E89E207 CRC64;

Query Match 32.7%; Score 413.5; DB 1; Length 250;
 Best Local Similarity 40.6%; Pred. NO. 1.2e-27;
 Matches 86; Conservative 35; Mismatches 82; Indels 9; Gaps 2;

QY 2 POKPKVSLNPPWNRIFKGENVTILTCNNGNFFVSTTKWFHNGSLGBETNSSLNIVNAKPE 61
 DB 23 PSKAVLLDPQWNHVLNDRVTILKCGDYPVEDNSTKWHNGTLLSSQTSPSYFIADVKVQ 82
 QY 62 DSCEYKCHQVNESEPVVLEFVSFVLLQASAEVVMGQPLFLCHGWNRWDVVKVIYY 121
 DB 83 DSCEYKCHQVNESEPVVLEFVSFVLLQASAEVVMGQPLFLCHGWNRWDVVKVIYY 142
 QY 122 KDCEALKVWENHNISITNATVEDSTYCTCTCKWQLDVSEPLNITVTKAPREKVMQLF 181
 DB 143 RNRGRKKYSHGNSDHPHPEAKLEHSGSVFCRIIGSKESSESVOITV-QAPETLQTVSS 201
 QY 182 FIP-----LLWVILFAVDLTGLFISTQQQV 205
 DB 202 FFPFPHQITFCLVMGVLFVAVDTGLYFSVRRHL 233

RESULT 5
 FC3A_HUMAN STANDARD; PRT; 254 AA.
 AC P08637;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor
 DE (IGG Fc receptor III-2) (Fc-gamma RIII-alpha) (Fc-gamma RIIIA)
 DE (FCRIIA) (FC-gamma RIII) (FCRIII) (CD16-A) (FCR-10).
 GN FCGR3A OR FCGR3 OR FCGR3 OR IGR3 OR CD16A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89328325; PubMed=2526846;
 RA Ravetch J.V., Petrusia B.;
 RT "Alternative membrane forms of Fc gamma RIII (CD16) on human natural
 RT killer cells and neutrophils. Cell type-specific expression of two
 RT genes that differ in single nucleotide substitutions.";
 RL J. Exp. Med. 170:481-497(1989).
 RN [2]
 RP SEQUENCE OF 1-39 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=95138131; PubMed=7836402;
 RA Gessner J.E., Grussermeyer T., Kolarus W., Schmidt R.E.;
 RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
 RT genes. Molecular characterization of the promoter regions.";
 RL J. Biol. Chem. 270:1350-1361(1995).
 RN [3]
 RP VARIANTS ARG-66 AND HIS-66.
 RX MEDLINE=96183251; PubMed=8609432;
 RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,
 RA van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;
 RT "A triallelic Fc gamma receptor type IIIA polymorphism influences the
 RT binding of human IGG by NK cell Fc gamma RIIIA.";
 RL J. Immunol. 156:3948-3955(1996).
 RN [4]
 RP VARIANT VAL-157.
 RX MEDLINE=97385047; PubMed=9242542;
 RA Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,
 RA de Haas M.;
 RT "Fc gammaRIIA-158V/F polymorphism influences the binding of IgG by
 RT natural killer cell Fc gammaRIIA, independently of the Fc
 RL gammaRIIA-48L/R/H phenotype.";
 RL Blood 90:1109-1114(1997).
 RN [5]
 RP VARIANT VAL-176.
 RX MEDLINE=97426467; PubMed=9276722;
 RA Wu J., Edberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,

Salmon J.E., Kimberly R.P.;
"A novel polymorphism of FcgammarIIa (CD16) alters receptor function
and predisposes to autoimmune disease.";
J. Clin. Invest. 100:1059-1070(1997).
-!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG.. BINDS COMPLEXED OR
CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT
RESPONSES, SUCH AS PHAGOCYTOSIS.
-!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC
EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists
also as a soluble receptor.
-!- TISSUE SPECIFICITY: Expressed on natural killer cells,
macrophages, subpopulation of T cells, immature thymocytes and
placental trophoblasts.
-!- PTM: Glycosylated. Contains high mannose- and complex-type
oligosaccharides.
-!- PTM: The soluble form is produced by a proteolytic cleavage.
-!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of
IgG1, IgG3 and IgG4 compared with isoform Phe-157. Alleles Leu-66
and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in
linkage disequilibrium.
-!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:
FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-
SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE
DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-!- DATABASE: NAME=PROW; NOTE=cd guide CD16a entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdl6a.htm".

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EMBL; X52645; CA36870.1; --
EMBL; Z46222; CA986295.1; --
FIR; JL0107; JL0107.
HSP; P12319; IALS.
Gene; HGNC:3619; FCGR3A.
MIM; 146740; --
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0006955; P:immune response; TAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
Pfam; PF00047; Ig; 2.
SMART; SMC0409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 16
FT CHAIN 17 254
FT FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT FT REGION RECEPTOR III-A.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT CYTOPLASMIC (POTENTIAL).
FT FT IG-LIKE C2-TYPE 1.
FT FT IG-LIKE C2-TYPE 2.
FT FT BY SIMILARITY.
FT FT BY SIMILARITY.
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT FT L -> R
FT FT /FTId=VAR_008799.
FT FT L -> H.
FT FT /FTId=VAR_008800.
FT FT F -> V.
FT FT VARIANT 157 157

```

/FTID=VAR_008801.
F> V (in dbSNP:396991).
/FTID=VAR_003960.
SEQUENCE 254 AA; 29089 MW; D38D178D32C67337 CR C64;
Query Match 32.6%; Score 411.5; DB 1; Length 254;
Best Local Similarity 41.6%; Pred. No. 1.7e-27;
Matches 87; Conservative 33; Mismatches 82; Indels 7; Gaps 1;

QY 4 KPKVSLNPWNRIKFGENTVLTFCNGNPFVEVSTKWFHNGSLSEETNSSLINVNAKFEDS 63
DB 25 KAVVLEPQWYRLEKSDSVTLKCOGAYSPEDSNTOFWHNESSLSQASSYFIDAAITVDD 84
QY 64 GRVKOHQVNSESEPVYLVESDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 123
DB 85 GEYRCOTNLSLSDPVLQEVHVGWLLLOAPRWVFKEDPIHLRCHSKWNTALHKVTYLN 144
QY 124 GEALKYWYENHNISITNATVEDSGTYCYCGKWQLDYSEPLNITWIKAPREKYWLQFFI 183
DB 145 GKGRKYFHNSDFYIPKATLKDSGYFCRGLFGSKNVSETVNTITITQGLAVSTISSFFP 204
QY 184 P-----LLVILFAVDYGLFISTQQOV 205
DB 205 PGVQSFCLVMVLLFAVDYGLYFSVKNI 233

RESULT 6
FCG3_PIG STANDARD; PRT; 257 AA.
ID FCG3_PIG Q28940; Q28941;
AC Q28942; Q28940; Q28941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (5G Fc receptor III) (Fc-gamma RIII) (FCRIII) (Cytolytic trigger
DE molecule G7).
DE DE
DE FCG3.
GS Sus scrofa (Pig).
OS Eukaryota; Metazoa;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
XN [ ]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
RP STRAIN=Minnesota miniature swine;
RC MEDLINE=94358430; PubMed=8077673;
RX Halloran P.J., Sweeney S.E., Strohmeier C.M., Kim Y.B.;
RT "Molecular cloning and identification of the porcine cytolytic
RT trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue.";
RT J. Immunol. 153:2631-2641(1994).
RL CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC CC -!- SUBUNIT: FORMS A COMPLEX WITH NK-E.
CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC CC -!- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PMNC,
CC MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
CC THYMUS OR LIVER.
CC CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U08993; AAA57190.1; -
DR EMBL; U08991; AAA57188.1; -
DR EMBL; U08992; AAA57189.1; -
DR HSRP; F12319; IALS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig 2.

```


CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD16B entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd16b.htm".
CC
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CC
CC ENBL; X16863; CAA34753.1; -
CC ENBL; X07934; CAA30758.1; -
CC ENBL; J04162; AAA35881.1; -
CC ENBL; Z46223; CAA86296.1; -
CC PIR; J00284; J00284.
CC PDB; 1E4J; 04-AUG-00.
CC PDB; 1E4K; 06-JUN-01.
CC PDB; 1FNU; 22-NOV-00.
CC PDB; 1IIS; 16-MAY-01.
CC PDB; 1IIX; 16-MAY-01.
CC PDB; 1IIX; 16-MAY-01.
CC Genew; HGNC:3620; FCGR3B.
CC GO; GO:0006955; P:Immune response; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; Ig; 2.
CC PROSITE; PSS0835; Ig-Like; 1.
CC IGG-binding protein; Receptor; GPI-anchor; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat; Multigene family; Polymorphism;
CC 3D-structure; Lipoprotein.
CC SIGNAL 1 16
CC CHAIN 17 200
CC
CC PROPEP 201 233
CC LIPID 200 200
CC DOMAIN 40 96
CC DOMAIN 121 179
CC DISULFID 47 89
CC DISULFID 128 172
CC CARBOHYD 56 56
CC CARBOHYD 63 63
CC CARBOHYD 82 82
CC CARBOHYD 92 92
CC CARBOHYD 180 180
CC CARBOHYD 187 187
CC VARIANT 36 36
CC
CC VARIANT 65 65
CC VARIANT 78 78
CC VARIANT 82 82
CC VARIANT 106 106
CC
CC SEQUENCE 233 AA; 26216 MW; 7AB5159432761726 CRC64;
Query Match 31.6%; Score 399.5; DB 1; Length 233;
Best Local Similarity 41.1%; Pred. No. 1.6e-26;
Matches 86; Conservative 32; Mismatches 84; Indels 7; Gaps 1;
QY 4 KPKVSLNPPWNRIFKGNVTLTCGNPNFFVSSTKWFNGSLSBETNSLNVNAKPEDS 63
DB 25 KAVVLEPQWYSLKESVTLKCGAYSPEDNSTQWFHNSLISSQASSYFIDAATVND 84
QY 64 GEYKCHQOVNESEPVYLEVSDWLLQASAEVMEGQPLFRCGHWENWVYKVIYKD 123
DB 85 GEYRCQTLNLTSLDFVQLEHIGWLLQAPRWVFKEDPIHLRCHSWKNTALHKVYLYQN 144
QY 124 GEALXVYENHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLPFI 183

Db 145 GKDRKYPFHNSDFHIPKATLKDSGYSYFCRGLVSGKNVSSVETVNIITITQGLAVSTISSFSP 204
QY 184 P-----LLVWVILFAVDITGLFISTQOQV 205
DB 205 PGYQVSCLVNVLLFAVDITGLYFSVKINI 233
RESULT 8
FCG3 RAT
ID FCG3 RAT STANDARD; PRT; 267 AA.
AC P27645; Q04798; Q63204;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).
GN FCGR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B; C AND D).
RC STRAIN-Sprague-Dawley;
RX MEDLINE=91250730; PubMed=1710249;
RA Farber D.L., Sears D.W.;
RT "Rat CD16 is defined by a family of class III Fc gamma receptors
RT requiring co-expression of heteroprotein subunits.";
RL J. Immunol. 146:4352-4361(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Natural killer cells;
RX MEDLINE=90239026; PubMed=1692135;
RA Zeger D.L., Hogarth P.M., Sears D.W.;
RT "Characterization and expression of an Fc gamma receptor cDNA cloned
RT from rat natural killer cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM H).
RC STRAIN-Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93246650; PubMed=8482840;
RA Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P.,
RA Sears D.W.;
RT "Rat class III Fc gamma receptor isoforms differ in Igg subclass-
RT binding specificity and fail to associate productively with rat CD3
RT zeta.";
RL J. Immunol. 150:4364-4375(1993).
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC -!- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS.
CC THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE
CC EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=8;
CC Comment=Additional isoforms seem to exist;
CC Name=C;
CC IsoId=P27645-1; Sequence=Displayed;
CC Name=A;
CC IsoId=P27645-3; Sequence=Not described;
CC Name=B;
CC IsoId=P27645-4; Sequence=Not described;
CC Name=D;
CC IsoId=P27645-5; Sequence=Not described;
CC Name=E;
CC IsoId=P27645-6; Sequence=Not described;
CC Name=F;
CC IsoId=P27645-7; Sequence=Not described;
CC Name=G;
CC IsoId=P27645-8; Sequence=Not described;
CC Name=H;
CC IsoId=P27645-2; Sequence=VSP_003647;
CC -!- TISSUE SPECIFICITY: EXPRESSED ON NATURAL KILLERS CELLS AND

CC CC MACROPHAGES.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -----
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 CC -----
 CC EMBL; M64368; AAA42049.1; -
 CC EMBL; M64369; AAA42048.1; -
 CC EMBL; M64370; AAA42050.1; -
 CC EMBL; M32062; AAA41148.1; -
 CC EMBL; L08446; AAA41151.1; -
 CC PIR; A35902; A35902.
 CC PIR; I56110; I56110.
 CC HSP; P12319; IALS.
 CC InterPro; IPR003599; IG-like.
 CC InterPro; IPR003599; IG.
 CC Pfam; PF00047; IG; 2.
 CC SMART; SM00409; IG; 2.
 CC PROSITE; PS50835; IG-LIKE; 2.
 CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Alternative splicing.
 FT SIGNAL 1 36
 FT CHAIN 37 267
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT REGION RECEPTOR III.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT SWKQKLTQVLLFQNGKPRVYVYSSNFSIPK -> GWKSI
 FT QKLRLSFLQNGEFVSHFYNVSISN (in isoform
 FT H).
 FT /FTID=VSP_002647.
 FT ANLP -> GDLL (IN ISOFORM A AND ISOFORM
 FT H).
 FT E -> D (IN ISOFORM A AND ISOFORM H).
 FT D -> G (IN ISOFORM D).
 FT V -> I (IN ISOFORM A AND ISOFORM B).
 FT E -> L (IN ISOFORM H).
 FT T -> R (IN ISOFORM H).
 FT N -> D (IN ISOFORM H).
 FT M -> E (IN ISOFORM H).
 FT K -> R (IN ISOFORM H).
 FT SEQUENCE 267 AA; 30281 MW; DD4D8A7A3F70ED92 CRC64;
 SQ
 Query Match 30.9%; Score 390; DB 1; Length 267;
 Best Local Similarity 37.9%; Pred. No. 1.2e-25;
 Matches 78; Conservative 40; Mismatches 84; Indels 4; Gaps 1;
 Qy 4 KPKVSLAPPNRIKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLIVNAKFEES 63
 Db 40 KAVVRDPFWITQVLKEDVTITTCGTHNPGNSSTGWQVQASYYTKFATVNS 99
 Qy 64 GEYKQHQVNESEPVYLVFSDWLLQLQASAEVMEQGPLFRCRGWRNDVTKVYVKD 123
 Db 100 GEYCRWAHTSLSPVHLEVISDWLLIQTPLQFEEGETITLRCHSKWKLTKVLLFQN 159
 Qy 124 GEALKYVHNISITWATVEDSTYCTCKWQLDVSEPLNITY-----IKAPREKYL 179
 Db 160 GKPVRYVYQSNFSIPKANHSHSGNYYCKAYLGRTHVSRKPVITVQGSATASSTSLVWF 219
 Qy 180 QFFPILLVILFAVDITGLFISTQCV 205.
 Db 220 HAAFLCWLCLFAVDITGLYFCVRNL 245

RESULT 9
 FC3_MOUSE STANDARD; PRT; 261 AA.
 AC P08508; 1988 (Rel. 08, Created).
 DT 01-AUG-1988 (Rel. 08, Last sequence update).
 DT 01-AUG-1988 (Rel. 08, Last annotation update).
 DT 10-OCT-2003 (Rel. 42, Last annotation update).
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor
 DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII).
 GN FCGR3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87042761; PubMed=2946078;
 RA Ravetch J.V., Luster A.D., Weinshank R., Kochan J., Pavlovic A.,
 RA Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
 RT "Structural heterogeneity and functional domains of murine
 RT immunoglobulin G Fc receptors.";
 RL Science 234:718-725(1986).
 RN [2]
 RP SEQUENCE OF 1-29 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Soares H.J., Onken M.D., Kulczycki A. Jr.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
 CC gamma. Low affinity receptor.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -----
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 CC -----
 CC EMBL; M14215; AAA37604.1; -
 CC EMBL; X60929; CAA43266.1; -
 CC PIR; S29360; S29360.
 CC HSP; P12319; IALS.
 CC MGD; MGI:95500; Fcgr3.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC Pfam; PF00047; Ig; 2.
 CC SMART; SM00409; Ig; 2.
 CC PROSITE; PS50835; IG-LIKE; 2.
 CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 30
 FT CHAIN 31 261
 FT POTENTIAL.
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
 FT REGION RECEPTOR III.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE 1.
 FT IG-LIKE C2-TYPE 2.
 FT BY SIMILARITY.
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 261 AA; 30036 MW; 757FB8368E41069 CRC64;
 SQ
 Query Match 30.7%; Score 387.5; DB 1; Length 261;
 Best Local Similarity 35.7%; Pred. No. 1.9e-25;
 Matches 84; Conservative 43; Mismatches 93; Indels 15; Gaps 5;
 Qy 4 KPKVSLAPPNRIKGENVTITCNGNFFVSSSTKWFHNGSLSEETNSLIVNAKFEED 62

34	KAVVYKLPPIQIVLKEDWTVLMCEGTHNPGNSSTQWFHNGRSIRSQVQASYTF-KATVND	92
63	SGEYKCOHQQVNGSEPEVYLVFSDWLLQLQASAVVNEGQPLFLRCHGWRNDWYKVIYVK	122
93	SGEYRCQMEQTRLSDPVDLGVISDWLLQLQPVRFLEGETITILRCHSWRNKLLNRISPFH	152
123	DGEALKYWEYHNHNIISINATVDSGTYCTGKTQWLDYSEBPLNTV----IKAPREXW	178
153	NEKSVRYHHYKSNFSIPKANHSHSGDYCKGSLGSHQSKPVTITVQDPATTSSISLW	212
179	LQFTPIPLVLVFAVDVTGLFISITQQQVTFLLKIKRTRKGRF---LNLPHKPNPK	230
213	YHTAFSLVMCLLFAVDVTGLFYVYR-----NLQTPREYWRKLSLRKHAQADK	261

Query Match	30.1%;	Score 381;	DB 1;	Length 296;
Best Local Similarity	41.2%;	Pred. No. 7.6e-25;		
Matches	70;	Conservative	33;	Mismatches 65;
				Indels 2;
				Gaps 1;

2 P Q K P X - - V S L N P P N R I F K G E N V T I T C N G N N F F E V S S T K W F H N G S L S E E T N S S L N I V N A K 59

60 FEDSEYKCHQVNESEPVVLEVFSDWLLQASAEVVMGQPLFIRCHGWRNDVYKVI 119

Db 104 SNDGSGRCQREQTSLESDPVEHLDVSDWLLLLQTPSLVYQEGEFLMCKRCHSWAKQFLNALI 169

QY 120 YYKDGALKVWYENHNISITNATVEDSGTYYCTGKWQLDYSEPLNITV 169

Db 164 FYQDRKSKI¹SYQRTNFSIPRANLSHSGQYHCTAFICKMLHSSQPVNITV 213

RESULT 11		
FCG1 HUMAN	FCG1 HUMAN	STANDARD; PRT; 374 AA.
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97	97	97
98	98	98
99	99	99
100	100	100

DT	01-OCT-1989	(rel. 12, Created)
DT	01-OCT-1989	(rel. 12, Last sequence update)
DT	10-OCT-2003	(rel. 42, Last annotation update)

DE High affinity immunoglobulin gamma Fc receptor 1 (CD64 antigen).
DE RI (FcRI) (IgG Fc receptor I) (CD64 antigen).
GN FCGR1A OR FCGR1 OR FCGR1 OR IGFR1.
GN Homo sapiens (Human)

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;

SEQUENCE FROM N.A.
MEDLINE=89098339; PubMed=2974947;
Allen J.M., Seed B.;

RT "Nucleotide sequence of three cDNAs for the human high affinity FC
RT receptor (FcRI).";
RT
RL Nucleic Acids Res. 16:11824-11824 (1988).

SEQUENCE FROM N.A.
MEDLINE=89100284; PubMed=2911749;
Allen J.M., Seed B.;

RT "Isolation and expression of functional high-affinity FC receptor complementary DNAs.";
RT Science 243:378-381(1989).
RL The action of immunoglobulin gamma High

CC affinity receptor.
CC
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -|- ALTERNATIVE PRODUCTS:

```
CC Event=Alternative splicing; Named Isoforms=2;
CC Name=A;
CC IsoId=P12114-1; Sequence=Displayed;
CC Name=B;
```

CC Isold=P12114-2; Sequence=VSP_002637;
CC
CC -| TISSUE SPECIFICITY: Monocyte/macrophage specific.
CC
CC -| SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

-I- DATABASE: NLM=PROW; NLM=CD guide esp. entry,
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd64.htm".

this swiss-spot entry is convright It is produced through a collaboration

[illegible][illegible]

RA Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
RT "Structural heterogeneity and functional domains of murine
RL immunoglobulin G Fc receptors."; Science 234:718-725(1986).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM IIB2).
RC TISSUE=Macrophage; PubMed=3024012;
RX MEDLINE=87065089; PubMed=3024012;
RA Lewis V.A., Koch T., Plutner H., Meilman I.;
RT "A complementary DNA clone for a macrophage-lymphocyte Fc receptor."; Nature 324:372-375(1986).
RL [3]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM IIB1).
RX MEDLINE=87306729; PubMed=2957319;
RA Hogarth P.M., Hibbs M.L., Bonadonna L., Scott B.M., Witort E.,
RA Pietersz G.A., McKenzie I.F.C.;
RT "The mouse Fc receptor for IgG (Iy-17): molecular cloning and
RN specificity."; Immunogenetics 26:161-168(1987).
RL [4]
RN SEQUENCE FROM N.A. (ISOFORM IIB1), AND VARIANTS.
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=90202030; PubMed=2138587;
RA Lah M., Quelch K., Deacon N.J., McKenzie I.F., Hogarth P.M.;
RT "Identification of the mouse beta Fc gamma RII polymorphism by direct
RN sequencing of amplified genomic DNA."; Immunogenetics 31:202-206(1990).
RL [5]
RN SEQUENCE FROM N.A. (ISOFORMS IIB1 AND IIB2).
RX MEDLINE=91079576; PubMed=1824594;
RA Hogarth P.M., Witort E., Hulet M.D., Bonnerot C., Even J.,
RA Fridman W.H., McKenzie I.F.C.;
RT "Structure of the mouse beta Fc gamma receptor II gene."; J. Immunol. 146:369-376(1991).
RL [6]
RN SEQUENCE FROM N.A. (ISOFORM IIB1').
RC STRAIN=DBA/2; TISSUE=Mast cells;
RX MEDLINE=96264690; PubMed=8683114;
RA Latour S., Fridman W.H., Daeron M.;
RT "Identification, molecular cloning, biologic properties, and tissue
RN distribution of a novel isoform of murine low-affinity IgG receptor
homologous to human Fc gamma RIIB1."; J. Immunol. 157:189-197(1996).
RL [7]
RN SEQUENCE OF 30-330 FROM N.A. (ISOFORMS IIB1 AND IIB2).
RC STRAIN=DBA/2, and NZB; TISSUE=Spleen;
RX MEDLINE=96128267; PubMed=8537115;
RA Sawchuk D.J., Mahmoudi M., Cairns E., Sinclair N.R.S.;
RT "Nonsynonymous mutations in an Fc-receptor structural gene in NZB
RN mice."; Immunogenetics 43:112-113(1995).
RL [8]
RN SEQUENCE OF 17-45 FROM N.A.
RX MEDLINE=96313694; PubMed=2944118;
RA Hibbs M.L., Walker I.D., Kirsbaum L., Pietersz G.A., Deacon N.J.,
RA Chambers G.W., McKenzie I.F.C., Hogarth P.M.;
RT "The murine Fc receptor for immunoglobulin: purification, partial
RN amino acid sequence, and isolation of cDNA clones."; Proc. Natl. Acad. Sci. U.S.A. 83:6980-6984(1986).
RL [9]
RN CHARACTERIZATION OF ISOFORM IIB3.
RC TISSUE=Macrophage;
RX MEDLINE=94001803; PubMed=8398981;
RA Tartour E., de la Salle H., de la Salle C., Teillaud C., Camoin L.,
RA Galinha A., Latour S., Hanau D., Fridman W.H., Sautes C.;
RT "Identification, in mouse macrophages and in serum, of a soluble
RN receptor for the Fc portion of IgG (Fc gamma R) encoded by an
alternatively spliced transcript of the Fc gamma RII gene."; Int. Immunol. 5:859-868(1993).
RL [10]
RN FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor. Involved in a variety of effector
CC gamma and regulatory functions such as phagocytosis of antigen-antibody
CC complexes from the circulation and modulation of antibody

CC production by B-cells. Isoform IIB1 and isoform IIB1' form caps
CC but fail to mediate endocytosis or phagocytosis. Isoform IIB2 can
CC mediate the endocytosis of soluble immune complexes via clathrin-
CC coated pits. Isoform IIB1 and isoform IIB2 can downregulate B-
CC cell, T-cell, and mast cell activation when coaggregated to B-cell
CC receptors for AG (BCR), T-cell receptors for AG (TCR), and Fc
CC receptors, respectively.
CC -!- SUBCELLULAR LOCATION: Type I
CC membrane protein. Isoform IIB1 binds the cytoskeleton and is not
CC localised in endocytotic pits. Isoform IIB3 is released as a
CC soluble molecule.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=IIB1; Synonyms=Beta-1;
CC IsoId=P08101-1; Sequence=Displayed;
CC Name=IIB2; Synonyms=Beta-2;
CC IsoId=P08101-2; Sequence=VSP_002640;
CC Name=IIB1'; Synonyms=Beta-1';
CC IsoId=P08101-3; Sequence=VSP_002641;
CC Name=IIB3; Synonyms=Beta-3;
CC IsoId=P08101-4; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: Widely expressed by cells of hemopoietic
CC origin. The isoforms are differentially expressed. Isoform IIB1 is
CC preferentially expressed by cells of the lymphoid lineage, isoform
CC IIB2 by cells of the myeloid lineage, and isoform IIB3 is released
CC by macrophages and is present in the serum. Isoform IIB1' is
CC expressed in myeloid and lymphoid cell lines, in normal spleen
CC cells, and in resting or LPS-activated B-cells but is not detected
CC in mesenteric lymph node cells.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC motif is involved in downmodulation of cellular responses. The
CC phosphorylated ITIM motif binds to the SH2 domain of FPN6/SHP-1.
CC Another tyrosine-containing sequence, more C-terminal, accounts
CC for the ability of isoform IIB2 to trigger the phagocytosis of
CC particulate immuno complexes.
CC -!- PTM: Glycosylated.
CC -!- PTM: When coaggregated to BCR, isoform IIB1 and isoform IIB1'
CC become tyrosine phosphorylated and bind to the SH2 domains of
CC the protein tyrosine phosphatase PTPC1.
CC -!- POLYMORPHISM: Ly-17 allelotypic system involves residues 116 and
CC 161. Ly-17.1 mice are Pro-116 and Glu-161; Ly-17.2 mice are Leu-
CC 116 and Leu-161. These polymorphisms do not affect IGG binding.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M16367; AAA37608.1; -
CC EMBL; M14216; AAA37609.1; -
CC EMBL; M17515; AAA37607.1; -
CC EMBL; M31312; AAA37610.1; -
CC EMBL; X04648; CAA28309.1; ALT_INIT.
CC EMBL; U31801; AAA92707.1; -
CC EMBL; U31802; AAA92708.1; -
CC EMBL; U31803; AAA92709.1; -
CC EMBL; U31804; AAA92710.1; -
CC EMBL; M14276; AAA37605.1; -
CC EMBL; U51629; AAA97464.1; -
CC PIR; B40071; FCMGSL.
CC MGD; MGI:95499; Fcgr2b.
CC GlycoSuiteDB; P08101; -
CC PIR; I49660; I49660.
CC GO; GO:0003793; F:defense/immunity protein activity; IMP.
CC GO; GO:0006955; P:immune response; IMP.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig; 2.
CC PROSITE; PS50835; IG_LIKE; 1.

RESULT 15	
FCG2_RAT	
ID_FCG2_RAT	STANDARD; PRT; 285 AA.
AC	O63203;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
DE	gamma RII) (FCRII) (IgG Fc receptor II beta).
GN	FCGR2.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;	
EN	[1]

QY	4	KPVSLNPPNRI	FKGENTVLT	CNGNFFPV	SVSTKWFH	NGSLSEET	NSLINI	VNAK	PEDS	63
Db	37	KAVKLEPP	QIQLKEDT	VTLMEG	HTKNCST	QWFHNG	SSLTHQ	CAQANY	TKATV	96
QY	64	GEYKCOHQ	QVNESE	PVLYE	VSFWLL	QASAEV	MEGQPL	FLRCHG	WRNDV	123
Db	97	GEYRCMEET	GISEPH	LGWISD	WLLQTS	QLVFE	GETITL	RCHSWK	NKQLAT	156
QY	124	GEALKYEN	HNHNSI	NAIVED	SGTYCT	CKWQLD	YSEPL	NI	TI	183
Db	157	GKPVRYHQ	SSNF	SIPKAN	SHSGNY	CKAYLGR	TMEVSK	PV	TI	211
QY	184	PLLWVI	189							
Db	212	PLVTIV	217							

Tue Oct 12 09:19:28 2004

us-10-763-400-6.rsp

Page 14

Search completed: October 6, 2004, 09:03:37
Job time : 8.84149 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      October 6, 2004, 08:59:40 ; Search time 36.5035 Seconds
              (without alignments)
              2005.293 Million cell updates/sec

Title:      US-10-763-400-6
Perfect score: 1264
Sequence:    1 VPQKTKVSLNPFPNFIKGE.....RTRKGFRLNPHPKPNPKNN 232

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:      1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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RESULT 1

QSMI30; AC
DDT DT
01-OCT-2002 (TREMBlrel. 22, Created)
01-OCT-2002 (TREMBlrel. 22, Last sequence update)
01-OCT-2003 (TREMBlrel. 25, Last annotation update)
with affinity immunoglobulin E receptor alpha subunit.

Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

A. -

STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;
MEDLINE=20424522; Pubmed=10970105;
MALLON C M Halliwell P F W Miller H R P

McAleese S.M., Halliwell R.E.W., Miller H.R.P.;
"Cloning and Sequencing of the horse and sheep high-affinity IGE
RT

receptor alpha chain cDNA.";
Immunogenetics 51:878-881(2000).

DR EMBL; Y18204; CAB40387.1; -
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.

DR pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.

DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 2.

DR FROSLIE; ES0833; IG_LIKE; 2
KW Immunoglobulin domain; Recept
SO SEQUENCE 255 AA: 29366 MW:

SEQ	SEQUENCE	255 AA;	29366 MW;	ASU659700684FBD8	CR604
SC 13;	score 785	5;	DB 6;	length	

Query Match	62.1%;	Score 785.5;	DB 6;	Length 255;
Best Local Similarity	66.2%;	Pred. No. 3.3e-63;		

Matches 151; Conservative 29; Mismatches 43; Indels 5; Gaps 2

Qy 3 QKPKVSLNPPNRI FKGENVT LTCNNPFEVSTKWFHNGSLSESTNSSLNIVNAKPED 62

28 RASTVSLNPPWPIFRGENVILTCNKNKPLKGNSTEWYNNITLTETVSSLNITNASHRS 87

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	785.5	62.1	255	6	Q8M130
2	743	58.8	260	6	Q8M020
3	409.5	32.4	254	6	Q8SPW2
4	398.5	31.5	280	4	Q92637
5	396	31.3	249	6	Q9N216
6	396	31.3	250	6	Q9N215
7	396	31.3	256	6	Q9N222
8	395.5	31.3	233	4	Q9UPY7
9	384.5	30.4	249	11	Q8B477
10	384	30.4	261	11	Q9S892
11	382.5	30.3	249	11	Q8B2R4
12	376.5	29.8	357	6	Q8SPW5
13	372	29.4	261	11	Q7RW99
14	371.5	29.4	374	4	Q92663
15	371	29.4	375	4	Q92495
16	369	29.2	330	11	Q8R142


```
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
DR RECEPTOR.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AB3D345C6 CRC64;

Query Match 31.5%; Score 398.5; DB 4; Length 280;
Best Local Similarity 36.7%; Pred. No. 5.1e-28;
Matches 79; Conservative 48; Mismatches 79; Indels 9; Gaps 3;

QY 4 KPVSLNPPMNRIFKGENVTLTCGNPNFFVSTKWFHNGSLSEETNSLNIVNAKFEES 63
DB 21 KAVITLQPPVSVFQETVTLHCEVHLPGSSSTQWFLNGTATQTSFYRITSASVND 80
QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFURCHGWRNWDVYKVIYKD 123
DB 81 GEYRCQGLSGRSDPTQLBIHRGWLQLQVSSRVFMEGEPLAURCHAWKDKLVNVLVYRN 140
QY 124 GEALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPR--EKYWLQF 181
DB 141 GRAKFFHNSNLTILKTNISNGTYHCSG-NQKHRYTSAGISQYTVGQLQPTPVWFHV 199
QY 182 FIPLLVLFAVDTGTFISTQQOQVTFLLKIKETRK 216
DB 200 LFYLAIGMFLNVTNLWVIRK-----LKRKKK 228

RESULT 5
Q9N216 PRELIMINARY; PRT; 249 AA.
AC Q9N216;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16.
DE GN CD16.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180233; PubMed=10713347;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline
RT Fc(gamma)RIIIA (CD16) homologue.";
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 31.3%; Score 396; DB 6; Length 249;
Best Local Similarity 39.4%; Pred. No. 7.4e-28;
Matches 84; Conservative 33; Mismatches 90; Indels 6; Gaps 1;

QY 4 KPVSLNPPMNRIFKGENVTLTCGNPNFFVSTKWFHNGSLSEETNSLNIVNAKFEES 63
DB 25 KAMVLEPEMNRVLVSDGVILKCEGAYPPGDNQAQWHNGSVIPHRAPSYSIEAARSEDS 84
QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFURCHGWRNWDVYKVIYKD 123
DB 85 GEYKCOQGLSASDPVQLVHTGWLLOAPRWVQEGDTQLRCHSKNKTQVKQVYFQD 144
QY 124 GEALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPR-----Y 177
DB 145 GEKGFPHKNSDFYIPKATSKHSGSYFCRGLIGNKSESEAVNITVQGPVPSTSTFLPH 204
QY 178 WLQFFIPLVILFAVDTGTFISTQQOQVTFLLK 210
DB 205 WYQIAFFLVTALLFVVDTGHLHVAVQRLQSSVK 237

RESULT 7
Q9N22 PRELIMINARY; PRT; 256 AA.
AC Q9N22;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16A.a'.
DE Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180233; PubMed=10713347;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline
RT Fc(gamma)RIIIA (CD16) homologue.";
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
SQ SEQUENCE 256 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 31.3%; Score 396; DB 6; Length 249;
Best Local Similarity 39.4%; Pred. No. 7.4e-28;
Matches 84; Conservative 33; Mismatches 90; Indels 6; Gaps 1;

QY 4 KPVSLNPPMNRIFKGENVTLTCGNPNFFVSTKWFHNGSLSEETNSLNIVNAKFEES 63
DB 24 KAMVLEPEMNRVLVSDGVILKCEGAYPPGDNQAQWHNGSVIPHRAPSYSIEAARSEDS 83
QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFURCHGWRNWDVYKVIYKD 123
DB 84 GEYKCOQGLSASDPVQLVHTGWLLOAPRWVQEGDTQLRCHSKNKTQVKQVYFQD 143
QY 124 GEALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKAPR-----Y 177
```

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF372453; AAK54249.1; -.
DR GO; GO:0003677; F-DNA binding; IEA.

DR GO; GO:0008170; F-N-methyltransferase activity; IEA.

DR GO; GO:0006306; P-DNA methylation; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR002052; N6_Mtase.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS00092; N6_MTASE; 1.

SQ SEQUENCE 256 AA; 28868 MW; B39D7D36D639CF44 CRC64;

Query Match 31.3%; Score 396; DB 6; Length 256;

Best Local Similarity 38.3%; Pred. No. 7.6e-28;

Matches 85; Conservative 42; Mismatches 81; Indels 14; Gaps 2;

QY 2 PQKPVSLNPPNRIKFGENVTLTCNGNNFPEVSTKWFHNGSLSEETNSLSINIVNAKPE 61

Db 23 PPKSVVILDPNDRLLKXSVTLKCGAYPPGDDSTERNWNTLSKNKASSYSDTAIVG 82

QY 62 DSGEYKQHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 121

Db 83 NSGEYTKTGLSAQSDPLRLVYKGLWLLQAPRWVQGESIRLCHTWNKNTITQKVQYF 142

QY 122 KDGEALKYVENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQF 181

Db 143 QNGKGFESHQNFYHPNATLKDGSGYFCRGITNTNLSSEAVKTVQGSKPSPLTSP 202

QY 182 FIP-----LLVILFAVDTGLFISTQQQVTFLLKIKRTRK 216

Db 203 FLPHQIIFCLVMGFLFAVDTGLYFSVR-----KVLRSK 237

RESULT 8

ID Q9UPY7 PRELIMINARY; PRT; 233 AA.

AC Q9UPY7;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE FC-gamma receptor IIIB (CD 16).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

EX MEDLINE=20487377; PubMed=11034564;

RA Watanabe Y., Shimada E., Fujiwara K., Niihara H., Shimano K.,

RA Mitsunaga S., Tadokoro K., Juji T.;

RT "Nucleotide sequence of a new FC gamma receptor IIIB allele that codes

for a neutrophil antigen."

RL Tissue Antigens 56:272-275(2000).

DR EMBL; AB025356; BAA83803.1; -.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Receptor.

FT VARIANT 54 54 K -> E.

SQ SEQUENCE 233 AA; 26215 MW; 74B51B90927B388 CRC64;

Query Match

Best Local Similarity 40.7%; Pred. No. 7.5e-28;

Matches 85; Conservative 33; Mismatches 84; Indels 7; Gaps 1;

QY 4 KPVKVLNPPNRIKFGENVTLTCNGNNFPEVSTKWFHNGSLSEETNSLSINIVNAKFE 63

Db 25 KAVVFLPEQWYSVLEKXSVTLKCGAYSPKDNSTOWFNHNSISSQASSYFIDAATVND 84

QY 64 GEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 123

Db 85 GEYRCQTNLSLSDPVQLEVHGWLLOAPRWVFKXEDPIHLRCHSWKNTALHKVYTLQN 144

QY 124 GEALKYVENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQFPI 183

Db 145 GKORKYFHNSDFHIPKATLKDGSGYFCRGLVGSKVNSSETVNTITQGLAVSTISSSP 204

QY 184 P-----LLVILFAVDTGLFISTQQQV 205

Db 205 PGVQVSFCLVWLLFAVDTGLYFSVKTNI 233

RESULT 9

Q8R477

ID Q8R477 PRELIMINARY; PRT; 249 AA.

AC Q8R477;

DT 01-JUN-2002 (Tremblrel. 21, Created)

DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Transmembrane receptor CD16-2.

GN FCRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL; TISSUE=Liver;

RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,

RA Taranin A.V.;

RT "Identification of CD16-2, a novel mouse receptor homologous to

CD16/FCGR3."

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF499613; AAM19249.1; -.

DR MGD; MGI:2179523; FCRL3.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR PROSITE; PS50835; IG_LIKE; 2.

KW Receptor.

SQ SEQUENCE 249 AA; 28382 MW; 3DEAF3D935BBF5CD CRC64;

Query Match 30.4%; Score 384.5; DB 11; Length 249;

Best Local Similarity 38.9%; Pred. No. 8.1e-27;

Matches 81; Conservative 38; Mismatches 78; Indels 11; Gaps 2;

QY 3 QPKVSLNPPNRIKFGENVTLTCNGNNFPEVSTKWFHNGSLSEETNSLSINIVNAKFE 62

Db 23 QKAVNLDPKVVRLVLESDVTLRCQGFSPEDNSIKWFHNSLIPHODANVITQSAVKD 82

QY 63 SGEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122

Db 83 SGMTRCQTALSTISDPVQLEVHGWLLOQTKWLFOEGDPIHLRCHSWQNRVRKVYTLQ 142

QY 123 DGEALKYVENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV-----IKAPRE 175

Db 143 NGKGYFHENSELPFKATHNDSGYSFCRLGHNNKSSASFRISLGDGSGSMFPP-- 200

QY 176 KYWLQFPIPLLVILFAVDTGLFISTQQ 203

Db 201 --WQITFCLLIGLLFAIDTGLVYFSVR 226

RESULT 10

Q9ES92

ID Q9ES92 PRELIMINARY; PRT; 261 AA.

AC Q9ES92;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor III.
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fossati Jimack L., Boucrot E., Izui S.;
RT "Mouse Fc gamma RIII: identification and characterization of a new
RL allele in C57BL/6 mice.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF197930; AAG28520.1; -.
DR EMBL; AK077227; BAC36696.1; -.
DR MGD; MGI:95500; Fcgr3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

Query Match 30.4%; Score 384; DB 11; Length 261;
Best Local Similarity 38.2%; Pred. No. 9.6e-27;
Matches 79; Conservative 39; Mismatches 84; Indels 6; Gaps 3;

QY 4 KPKVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNSGSLSEETNSLINVNAKPED 62
DB 34 KAVVLDPPWIVQLKEDVTLKCEGTHNPGNSSTQWFHNSIRSQVSSYTF-KATVND 92
QY 63 SGEYKCOHQVNESEPVYLEVFDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122
DB 93 SGEYRCQMEQLSDPDVLDGIVSDWLLLOQTPQVLEGETITLURCHSWRNKLNISFFH 152
QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITV-----IKAPRE 178
DB 153 NEKSVRHHYKSNFSPKANHSQDYCKSLGSGTQHQSKPTIIVQDPATTSSISLW 212
QY 179 LQFFIPLLVILFAVDTGLFISTQQV 205
DB 213 YHTAFSLVMCLLFAVDTGLFYVVRNL 239

RESULT 11
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AC Q8R2R4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL
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DR EMBL; BC027310; AAH27310.1; -.
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DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
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QY 63 SGEYKCOHQVNESEPVYLEVFDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122
DB 83 SGMVRCQPTALSTISDPVQLEVHMGWLLLTQTKWLFQEGDPIHLRCHSWQRNRPVKVYSQ 142
QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITV-----IKAPRE 175
DB 143 NGKGGKYPHENSELLIPKATHENDSGSYFCRGLIGHNNKSSASFRISLGDGPGSPMFFP-- 200
QY 176 KYWLQFFIPLLVILFAVDTGLFISTQQ 203
DB 201 --WHQITFCLLIGLLFAIDTVLYFSVRR 226

RESULT 12
Q8SPW5 ID Q8SPW5 PRELIMINARY; PRT; 357 AA.
AC Q8SPW5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor 1.
GN FCGR1.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Macaca.
CX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nameruk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA Presta L.G.;
RT "Binding of human IgG to cynomolgus FcR.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485812; AAL32095.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Receptor.
SQ SEQUENCE 357 AA; 40715 MW; F5C51A06A3BCB08F CRC64;

Query Match 29.8%; Score 376.5; DB 6; Length 357;
Best Local Similarity 41.0%; Pred. No. 6.9e-26;
Matches 68; Conservative 36; Mismatches 61; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNSGSLSEETNSLINVNAKPEDS 63
DB 21 KAVITLQPPFWVSFQETVTLQCEVRLPGSSSTQWFLNGATQTSTPSYRITSASVKDS 80
QY 64 SGEYKCOHQVNESEPVYLEVFDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 123
DB 81 GEYRCQSGRSDPIQLEIHRDNLQVSRVFTGEFPLALRCHAWKDLVYVLYYQN 140
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QY 124 GEALKYWNENHISITNATVDSGTYYCTGKQWQDYSEPLNITV 169
DB 141 GKAFKFFYNSQLTILKTNISHNGAYHCSG-MGKHRYTSAGSVTV 185

RESULT 13
Q7TW9
ID Q7TW9 PRELIMINARY; PRT; 261 AA.
AC Q7TW9;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to Fc gamma receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerk A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RW EMBL; BC052819; AAH52819.1; -.
KW Receptor.
SQ SEQUENCE 261 AA; 30032 MW; 81389D45C2E14730 CRC64;

Query Match 29.4%; Score 372; DB 11; Length 261;
Best Local Similarity 37.7%; Pred. No. 1.2e-25;
Matches 78; Conservative 38; Mismatches 85; Indels 6; Gaps 3;

QY 4 KPKVSLNPPNRIKFGENVTLTCGNFFVSVSTKWFHN-GSLSEBTSNLSLVNAKFD 62
DB 34 KAVVLPDPPIQVLKEDNVTLMCEGTHNPONSSTQWFHNSIRSQSSYTF-KATVND 92
QY 63 SGXEYKCHQVNESEPYLLEFVSDWLLQLQASAEVVMGQPLFRCGHRNNDVYKVIYK 122
DB 93 SGYRCQMEQTRLSDPVDLGVISDWLLLPQFVLEGETITLRCPSWRNKLNRISPFH 152
QY 123 DGEALKYWNENHISITNATVDSGTYYCTGKQWQDYSEPLNITV----TKAPEKTV 178
DB 153 NEKSVRYHHYKSNFSPKANHSHSGDYKCKSLGSGTQHSQKPVITIVQDPATTSSISLV 212
QY 179 LQFFIPLLVILFAVDTLGLFISTQQVQ 205
DB 213 HHTAFSLVMCLLFAVDIGLYFYVRNL 239

RESULT 14

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Q92663
ID Q92663 PRELIMINARY; PRT; 374 AA.
AC Q92663;
DT 01-FEB-1997 (TremBLrel. 02, Created)
DT 01-FEB-1997 (TremBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fc gamma receptor I.
GN Al.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Forges A.J., Redecha P.B., Doebele R., Fan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109 (1992).
DR EMBL; L03418; AAA36049.1; -.
DR FIR; A39878; A39878.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 374 AA; 42632 MW; D33D59398CEBA699 CRC64;

Query Match 29.4%; Score 371.5; DB 4; Length 374;
Best Local Similarity 41.0%; Pred. No. 2.1e-25;
Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPNRIKFGENVTLTCGNFFVSVSTKWFHNSLSEETSSNLSLVNAKFD 63
DB 21 KAVITLQPPWVSFQEEVTTLHCEVLHPGSSSTQWFLNGTATQTSTPSYRITSASVND 80
QY 64 GEYKCHQVNESEPYLLEFVSDWLLQLQASAEVVMGQPLFRCGHRNNDVYKVIYK 123
DB 81 GEYRCQGLSGRSDPIQLIHRGWLLQVSRVTEGEPLALRCHANKDKLVNVLVYRN 140
QY 124 GEALKYWNENHISITNATVDSGTYYCTGKQWQDYSEPLNITV 169
DB 141 GKAFKFFHNSNLTKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 15
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AC Q92495;
DT 01-FEB-1997 (TremBLrel. 02, Created)
DT 01-FEB-1997 (TremBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Fc gamma receptor type I (Fc gamma RIB=Fc gamma receptor).
GN CD64 OR FC-GAMMA-RIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Ravesh D.,
RA Ezekowitz A.B.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-224 FROM N.A.
RX MEDLINE=93018627; PubMed=1402657;
RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Ravesh D.P.,
RA Ezekowitz R.A.;

```


RT "Definition of interferon gamma-response elements in a novel human Fc gamma receptor gene (Fc gamma R1b) and characterization of the gene

RT	"Definition of interferon gamma- gamma receptor gene (Fc gamma R1b structure.";	J. Exp. Med. 176:11115-1123(1992).	
RT	EMBL;	M91155; AAA58414.1; -	
RT	EMBL;	M91150; AAA58414.1; JOINED.	
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DR	EMBL;	S45704; AD113842.1; JOINED.	
DR	EMBL;	S45705; AD113842.1; JOINED.	
DR	InterPro; IPR001710; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	Pfam; PF00047; Ig; 3.		
DR	SMART; SM00408; IGG2; 1.		
DR	PROSITE; PS5083; IG_LIKE; 3.		
DR	Immunoglobulin domain.		
DR	SEQUENCE 375 AA; 42881 MW; AS		

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GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	699	100.0	1081	9	HOMMC1A	U03605 Human mast
8	699	100.0	1102	9	BC005912	BC005912 Homo sapi
9	699	100.0	1174	6	ARI123794	ARI123794 Sequence
10	699	100.0	1198	6	ARI175479	ARI175479 Sequence
11	699	100.0	1198	6	ARI175480	ARI175480 Sequence
12	699	100.0	1198	6	ARI74287	AX074287 Sequence
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ALIGNMENTS

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ACCESSION ARI75483
VERSION ARI75483.1 GI:17916782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 699)
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE Method to detect IGE
JOURNAL Patent: US 6309832-A 7 30-OCT-2001;
FEATURES Location/Qualifiers

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ORIGIN	ORIGIN	ORIGIN
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VERSION	AR175481.1	AR175482.1
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SOURCE	Unknown.	Unknown.
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AUTHORS	Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.	Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE	Method to detect IGE	Method to detect IGE
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VERSION A21606.1 GI:579605
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PN JP 2002531086-A/8
PD 24-SEP-2002
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 Shimizu,A., Tepler,I., Benfey,P.N., Berenstein,E.H.,
 Siraganian,R.P. and Leder,P.
 Human and rat mast cell high-affinity immunoglobulin E receptors:
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 BC005912
 BC005912.1 GI:13543505
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 Homo sapiens (human)
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 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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 Strausberg, R.
 Direct Submission
 Submitted (02-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC) Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>
 Series: IRAL Plate: 21 Row: h Column: 16
 This clone was selected for full length sequencing because it
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 DEFINITION Sequence 10 from patent US 6171803.
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 VERSION ARI23794.1 GI:14109155
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 ORGANISM Unknown.
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 Kinet, J. Pierre.
 TITLE Isolation, characterization, and use of the human .beta. subunit of
 the high affinity receptor for immunoglobulin E
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VERSION	AX074287.1	AX074287.1						

KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1
AUTHORS	Weber, F.R., Wood, K.V. and Hall, M.P.
TITLE	Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof
JOURNAL	Patent: WO 0104310-A 1 18-JAN-2001;
	Heska Corporation (US); PROMEGA CORPORATION (US)

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ACCESSION	AX074289
VERSION	AX074289.1 GI:12710476
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
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REFERENCE 1
AUTHORS Weber, E.R., Wood, K.V. and Hall, M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 3 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
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DEFINITION Sequence 7 from Patent WO0121816.
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ACCESSION AX101304.1 GI:13620094
VERSION

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REFERENCE 1
AUTHORS Kinet, J.P., Donnadieu, E., Jouvin, M.H., Cookson, W. and Moffatt, M.F.
TITLE Modulation of ige receptor cell surface expression
JOURNAL Patent: WO 0121816-A 7 29-MAR-2001;
ISIS INNOVATION LIMITED (GB); Beth Israel Deaconess Medical Center, Inc. (US)
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ACCESSION AX335621
VERSION AX335621.1 GI:18126340
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6130 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Best Local Similarity 100.0%; Pred. No. 7.7e-199;
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DB 722 TTTTATATCCATTTGTTGGTGAATTCGTTTGTGTGGACACAGGATTTATCTCA 781
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DB 782 ACTCAGCAGCAGTCACTTCTCTTCAAGATTAAAGAACAGGAAGGCTTCAGACTT 841
QY 661 CTGAACCCACATCCTAAGCCAAACCCCAAACTGA 699
|||||

Db 842 CTGAACCCACATCCTTAAGCCAAACCCCAAACTGA 880

Search completed: October 10, 2004, 16:11:55
Job time : 3044.74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 339.879 Seconds
(without alignments)
8736.904 Million cell updates/sec

Title: US-10-763-400-7
Perfect score: 699
Sequence: 1 GTCCTCGAGAACCTAAGT.....CAAAACCCCAAAACAACCTGA 699

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues 6747726
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001s:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	699	100.0	774	4	Aaf97964 Human imm
2	699	100.0	1068	3	Aaa27470 Human Fc
3	699	100.0	1088	1	Aan90126 cDNA enco
4	699	100.0	1174	2	Aag51020 Human Fce
5	699	100.0	1197	2	Aat85615 Alpha sub
6	699	100.0	1198	2	Aav36343 cDNA enco
7	699	100.0	1198	3	Aaa34813 Human ade
8	699	100.0	1198	3	Aaf20935 Human hig
9	699	100.0	1198	4	Aaf77692 Human wil
10	699	100.0	1198	5	Aaf24912 Complemen
11	699	100.0	1198	5	Aaf24911 Nucleotid
12	699	100.0	1198	6	AbL67793 Oesophagu
13	699	100.0	1198	7	Abz96629 Human hig
14	699	100.0	1198	9	AdB85535 Human imm
15	699	100.0	21742	3	Aaa34816 Human ade
16	699	100.0	21742	7	Aaf20938 Human hig
17	699	100.0	21742	7	Abz96632 Human hig
18	699	100.0	117608	7	Abz97129 Human rec
19	699	100.0	117609	3	Aaf21435 Human rec
20	698	99.9	773	6	AbS52959 Human cdn
21	697.4	99.8	898	8	AcD06182 Human cdn
22	696.4	99.6	773	2	Aav20402 Human IGE
23	696	99.6	696	5	Aaf24914 Complemen

24	696	99.6	696	5	Aaf24913 Nucleotid
25	695.8	99.5	1193	2	AaQ04644 Encodes a
26	695.8	99.5	1199	2	AaQ14736 Human Fc(
27	547	78.3	570	3	Aaa27472 Recombina
28	540.8	77.4	1150	2	AaQ34840 Human hig
29	537.8	76.9	2955	2	AAV20404 Plasmid R
30	537.8	76.9	2955	6	AbS52957 Human CDN
31	534	76.4	851	2	AaQ27267 Human FCE
32	528	75.5	528	3	Aaa27301 Human Fce
33	528	75.5	528	4	Aah47768 Nucleotid
34	516	73.8	516	3	Aaa27302 Human nhf
35	516	73.8	516	5	Aaf24917 DNA enco
36	516	73.8	516	5	Aaf24918 Complemen
37	516	73.8	516	5	Aaf24915 DNA enco
38	516	73.8	591	5	Aaf24916 Complemen
39	516	73.8	713	2	AaQ55969 Human dih
40	516	73.8	1908	5	Aaf24929 Fc epsilo
41	516	73.8	1908	5	Aaf24928 Fc epsilo
42	516	73.8	1983	5	Aaf24927 Fc epsilo
43	516	73.8	1983	5	Aaf24926 Fc epsilo
44	516	73.8	2193	5	Aaf24923 Complemen
45	516	73.8	2268	5	Aaf24921 Complemen

ALIGNMENTS

RESULT 1
AAF97964
ID AAF97964 standard; cDNA; 774 BP.

AC AAF97964;
XX

DT 19-JUN-2001 (first entry)

DE Human immunoglobulin E receptor I alpha subunit coding sequence.

XX Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGRA;
KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
KW immunoassay; detection; ss.

XX Homo sapiens.

XX WO20011010-A2.

XX 15-FEB-2001.

XX 02-AUG-2000; 2000WO-US021097.

XX 09-AUG-1999; 99US-0147860P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
PI Stephens JC;

XX WPI; 2001-202766/20.

XX P-PSDB; AAB74667.

XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms
in the immunoglobulin E receptor I alpha subunit gene.

XX Claim 7; Fig 2; 99pp; English.

XX The present invention describes an isolated polynucleotide (I) comprising
a nucleotide sequence (S) which is a polymorphic variant of a reference
sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
gene or its fragment. The polymorphic variant comprises at least one
polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
(A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at

CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGRA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGRA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGRA gene PCR primers which are used in
 CC the exemplification of the present invention. The present sequence
 CC encodes the human IGRA protein used in the present invention
 XX
 SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 699; DB 4; Length 774;
 Best Local Similarity 100.0%; Pred. No. 5.7e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 Db 76 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 135
 QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
 Db 136 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 195
 QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTGTAATATGTCGATGCAATTT 180
 Db 196 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTGTAATATGTCGATGCAATTT 255
 QY 181 GAAGACAGTGAGAAATCAAAATGTGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
 Db 256 GAAGACAGTGAGAAATCAAAATGTGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 315
 QY 241 CTGGAAGTCTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGTGGTATGAGGGC 300
 Db 316 CTGGAAGTCTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGTGGTATGAGGGC 375
 QY 301 CAGGCTCTCTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGTGGTATGAGGGC 360
 Db 376 CAGGCTCTCTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGTGGTATGAGGGC 435
 QY 361 TATAGAGTGGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420
 Db 436 TATAAGGATGGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 495
 QY 421 GCCACAGTTGAAGACAGTGAACCTCTACTGTACGGGAAAGTGGCAGCTGGACTAT 480
 Db 496 GCCACAGTTGAAGACAGTGAACCTCTACTGTACGGGAAAGTGGCAGCTGGACTAT 555
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAGAAGTACTGGCTACAA 540
 Db 556 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCTCCGCGTGAGAAGTACTGGCTACAA 615
 QY 541 TTTTATATCCATTTGTTGGTGTGATCTGTTGCTGTGGACACAGATATTATCTCA 600
 Db 616 TTTTATATCCATTTGTTGGTGTGATCTGTTGCTGTGGACACAGATATTATCTCA 675
 QY 601 ACTCAGCAGCAGGTCACTTTCTTTGAGATTAAGAGAACCAAGGAAAGGCTTCAGACTT 660
 Db 676 ACTCAGCAGCAGGTCACTTTCTTTGAGATTAAGAGAACCAAGGAAAGGCTTCAGACTT 735
 QY 661 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACAACTGA 699
 Db 736 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 2

AAA27470

ID AAA27470 standard; cDNA; 1068 BP.

XX

AC AAA27470;
 XX 11-SEP-2000 (first entry)
 DT Human Fc receptor, FcpsilonRia, coding sequence.
 XX Human Fc receptor, FcpsilonRia, coding sequence.
 DE Human; Fc receptor; FcpsilonRia; immunoglobulin; infection;
 KW immune response; HIV; IgG; immunosuppressive; antirheumatic;
 KW antinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
 KW systemic lupus erythematosus; tumour; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 31.813
 CDS /*tag= a
 FT /product= "FcpsilonRia"
 FT
 XX EP1006183-A1.
 XX 07-JUN-2000.
 PD 03-DEC-1998; 98EP-00122969.
 PF 03-DEC-1998; 98EP-00122969.
 PR 03-DEC-1998; 98EP-00122969.
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA
 XX WPI: 2000-367968/32.
 DR P-PSDB; AAF96230.
 XX Novel Fc receptor lacking transmembrane domains, a signal peptide, and
 PT glycosylation, useful for diagnosing and treating immune disorders and
 PT cancer.
 PT
 PS Disclosure; Page 17; 60pp; English.
 XX The present sequence is the human Fc receptor, FcpsilonRia, coding
 CC sequence. Fc receptors play a key role in defending the body against
 CC infections. First, pathogens are opsonised by serum immunoglobulins. The
 CC resulting complex then binds to cells expressing Fc receptors. Upon Fc
 CC receptor activation, immune effector pathways are activated, leading to
 CC immune response. The present sequence may be modified to produce
 CC recombinant versions. The recombinant Fc receptor consist only of the
 CC extracellular portion of the receptor and are not glycosylated i.e. they
 CC do not have transmembrane domains or signal peptides. The recombinant
 CC proteins may be used in immunoassays to determine the immune status of
 CC patients with chronic diseases of the immune system, e.g. AIDS, systemic
 CC lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid
 CC arthritis. In addition, pharmaceutical compositions containing
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM
 XX
 SQ Sequence 1068 BP; 330 A; 215 C; 229 G; 294 T; 0 U; 0 Other;
 Query Match 100.0%; Score 699; DB 3; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 6.7e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 Db 115 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 174
 QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
 Db 175 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 234
 QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTGTAATATGTCGATGCAATTT 180
 Db 235 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTGTAATATGTCGATGCAATTT 294
 QY 181 GAAGACAGTGAGAAATCAAAATGTGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240

Db 295 GAAGACAGTGGAGATACAAATGTCTGACGACCAACAAAGTTAATGAGTGAACCTGTGTAC 354
QY 241 CTGGAAAGTCTTCAGTGACTGGTGTCTCTTCAGGCTCTGCTGAGGTGTGTGAGGAGGC 300
Db 355 CTGGAAAGTCTTCAGTGACTGGTGTCTCTTCAGGCTCTGCTGAGGTGTGTGAGGAGGC 414
QY 301 CAGCCCTCTTCCTCAGGTGCTGATGCTGAGGAACTGGGATGTGTACAGGTGTATCTAT 360
Db 415 CAGCCCTCTTCCTCAGGTGCTGATGCTGAGGAACTGGGATGTGTACAGGTGTATCTAT 474
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACTCTCCATTACAAAT 420
Db 475 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACTCTCCATTACAAAT 534
QY 421 GCCACAGTTGAACACAGTGGAACTTACTGTCTGCGGCAAAAGTGTGGCAGCTGGACTAT 480
Db 535 GCCACAGTTGAACACAGTGGAACTTACTGTCTGCGGCAAAAGTGTGGCAGCTGGACTAT 594
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTTACAA 540
Db 595 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTTACAA 654
QY 541 TTTTATATCCATGTTGGTGGTATCTGTGTTGCTGTGTGGAACACAGGATTTATCTCA 600
Db 655 TTTTATATCCATGTTGGTGGTATCTGTGTTGCTGTGTGGAACACAGGATTTATCTCA 714
QY 601 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 660
Db 715 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 774
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 775 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 813

RESULT 3
ID AAN90126
XX AAN90126 standard; cDNA; 1088 BP.
AC AAN90126;
XX AC
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX XX
DE cDNA encoding human mast cell IgE receptor alpha subunit.
XX cDNA; immunoglobulin E receptor alpha subunit; treats allergies;
KW design non-peptide drugs; human.
XX Homo sapiens; (Human); mast cell line.
OS KU812.
XX Key Location/Qualifiers
PH 35..805
FT CDS /*tag= a
FT FT
XX W08905352-A.
XX FN
XX 15-JUN-1989.
XX PD
XX 29-NOV-1988; 88WO-US004255.
XX PF
XX 01-DEC-1987; 87US-00127214.
XX PR
XX (HARD) HARVARD COLLEGE.
XX PA (USSH) NAT INST OF HEALTH.
XX PA
XX Leder P, Benfey P;
XX PI
XX WPI; 1989-192698/26.
XX DR
XX P-PSDB; AAP90385.
XX DT

PT CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX Disclosure; Fig 4; 17pp; English.
XX
CC CDNA sequence encoding immunoglobulin E receptor alpha subunit of human
CC mast cell IGE surface receptor (see corresp. AAP90385). Used to produce
CC antibodies which can diagnose IGE receptor levels, measure and treat
CC allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1088 BP; 347 A; 216 C; 229 G; 296 T; 0 U; 0 Other;
Query Match 100.0%; Score 699; DB 1; Length 1088;
Best Local Similarity 100.0%; Pred. No. 6.8e-200;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAAACCTTACAGTCTCTTGAACCTCCATGGATAGAAATTTAAAGGAGAG 60
Db 110 GTCCCTCAGAAACCTTACAGTCTCTTGAACCTCCATGGATAGAAATTTAAAGGAGAG 169
QY 61 AATGTGACTCTTACATGTATATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 120
Db 170 AATGTGACTCTTACATGTATATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGTTTC 229
QY 121 CACAATGGCAGCCTTTGAGAAAGACAAATTCAGATTGTAATATGTAATGCCAAATTT 180
Db 230 CACAATGGCAGCCTTTGAGAAAGACAAATTCAGATTGTAATATGTAATGCCAAATTT 289
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 290 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 349
QY 241 CTGGAAGTCTTTCAGTGACTGCTGCTCTCAGGCTCTGCTGAGGCTGTGATGAGAGGC 300
Db 350 CTGGAAGTCTTTCAGTGACTGCTGCTCTCAGGCTCTGCTGAGGCTGTGATGAGAGGC 409
QY 301 CAGCCCTCTTCTCAGTGCCTGCTGCTGAGGAGGAGTGGGATGTGTACAAGTGTATCTAT 360
Db 410 CAGCCCTCTTCTCAGTGCCTGCTGCTGAGGAGGAGTGGGATGTGTACAAGTGTATCTAT 469
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACTCTCCATTACAAAT 420
Db 470 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAACTCTCCATTACAAAT 529
QY 421 GCCACAGTTGAACACAGTGGAACTTACTGTCTGCGGCAAAAGTGTGGCAGCTGGACTAT 480
Db 530 GCCACAGTTGAACACAGTGGAACTTACTGTCTGCGGCAAAAGTGTGGCAGCTGGACTAT 589
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 540
Db 590 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 649
QY 541 TTTTATATCCATGTTGGTGGTATCTGTTTGTGTGTGACACAGGATTTATCTCA 600
Db 650 TTTTATATCCATGTTGGTGGTATCTGTTTGTGTGTGACACAGGATTTATCTCA 709
QY 601 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 660
Db 710 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 769
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 770 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 808

RESULT 4
ID AAN90126
XX AAN90126 standard; DNA; 1174 BP.
XX AC AAN90120;
XX AC
XX 25-MAR-2003 (revised)
DT 21-JUN-1994 (first entry)
DT

XX DE Human FcεRI alpha gene.
 XX KW IgE; immunoglobulin E receptor; beta subunit; basophils; allergy;
 XX KW aggregation; signal transduction; diagnosis; antagonist; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 107..881
 XX FT /*tag= a
 XX FT
 XX PN WO9321317-A1.
 XX PD 28-OCT-1993.
 XX PF 16-APR-1993; 93WO-US003419.
 XX PR 16-APR-1992; 92US-00869933.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX PI Kinet JP;
 XX DR WPI; 1993-351727/44.
 XX DR P-PSDB; AAR42336.
 XX PT Immunoglobulin E receptor human beta sub-unit isolation - using 1st
 XX PT strand reverse transcripts from human basophils as templates for a
 XX PT polymerase chain reaction, used to treat and diagnose allergic diseases.
 XX PS Claim 1; Fig 1; 154pp; English.
 XX SS The sequence is that of the human FcεRI alpha subunit, isolated by using
 CC first strand reverse transcriptase from human basophils by PCR. The gene
 CC and its prod. can be used to identify human beta subunit FcεRI inhibitors
 CC (immunoglobulin E receptor) which inhibit the binding of IgE to its
 CC receptor and inhibit the aggregation function of the receptor or the
 CC signal transducing function related to allergic response. Such inhibitors
 CC can be used for the treatment or prevention of allergic disease. See also
 CC AA051021-4. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 1174 BP; 378 A; 240 C; 241 G; 315 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 2; Length 1174;
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACTCAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
 DB 182 GTCCTCAGAACTCAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 241
 QY 61 AATGTGACTCTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
 DB 242 AATGTGACTCTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 301
 QY 121 CACAAATGCGAGCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 180
 DB 302 CACAAATGCGAGCTTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 361
 QY 181 GAAGACAGTGGAGAAATCAAAATGTGACACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
 DB 362 GAAGACAGTGGAGAAATCAAAATGTGACACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 421
 QY 241 CTGGAAGTCTTCACTGACTGGTCTCTTCAGGCTCTCTGAGGTGGTGGAGGCG 300
 DB 422 CTGGAAGTCTTCACTGACTGGTCTCTTCAGGCTCTCTGAGGTGGTGGAGGCG 481
 QY 301 CAGCCCTCTTCTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTAT 360
 DB 482 CAGCCCTCTTCTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTAT 541
 QY 361 TATAGGATGGTGNAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

DB 542 TATAGGATGGTGNAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 601
 QY 421 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGTGGACTAT 480
 DB 602 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGTGGACTAT 661
 QY 481 GAGTCTGAGCCCTCAACATTAATTAAGCTCCGCTGAGAGTACTGGCTCAAA 540
 DB 662 GAGTCTGAGCCCTCAACATTAATTAAGCTCCGCTGAGAGTACTGGCTCAAA 721
 QY 541 TTTTATATCCCATTTGTTGGTGGTGAATCTCTGTTGGACACAGGATTTATCTCA 600
 DB 722 TTTTATATCCCATTTGTTGGTGGTGAATCTCTGTTGGACACAGGATTTATCTCA 781
 QY 601 ACTCAGCAGCAGTGCACATTTCTCTGAAGATTAAAGAACCCGAAAGGCTTCAGACTT 660
 DB 782 ACTCAGCAGCAGTGCACATTTCTCTGAAGATTAAAGAACCCGAAAGGCTTCAGACTT 841
 QY 661 CTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTGA 699
 DB 842 CTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTGA 880

RESULT 5
 AAT85615
 ID AAT85615 standard; cDNA; 1197 BP.
 XX AC AAT85615;
 XX DT 04-FEB-1998 (first entry)
 XX DE Alpha subunit of human high affinity receptor for IgE (human FcεRI) cDNA.
 KW alpha subunit; human high affinity receptor; IgE; FcεRI; antigen;
 KW preformed mediator; histamine; serotonin; leukotriene; IgE level;
 KW allergic condition; therapy; allergic response; drug screening;
 KW DNA probe; diagnostic assay; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 106..880
 XX FT /*tag= a
 XX FT /product= "human_FcεRI_alpha_subunit"
 XX FT sig_peptide 106..181
 XX FT /*tag= b
 XX FT mat_peptide 182..877
 XX FT /*tag= c
 XX FT /product= "alpha_subunit"

US5639860-A.
 17-JUN-1997.
 24-FEB-1988; 88US-00160457.
 24-FEB-1988; 88US-00160457.
 (USSH) US DEPT HEALTH & HUMAN SERVICES.
 (HOFF) HOFFMANN LA ROCHE INC.
 Kochan JP, Kinet JP;
 WPI; 1997-332052/30.
 P-PSDB; AAW24066.

DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
 E - used for producing polypeptide(s) which can be used for therapy or to
 prevent allergic responses or in diagnostic and screening assays.
 Claim 1; Fig 1A-B; 15pp; English.

CC This cDNA sequence encodes the alpha subunit of the human high affinity
CC receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC triggers both the release of of preformed mediators such as histamine and
CC serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC the release of these mediators that results in an allergic condition. The
CC DNA can be used to produce the human FcERI alpha polypeptides which can
CC be used for therapy or to prevent allergic responses, in drug screening
CC assays or for monitoring IgE levels in patients. The DNA can also be used
CC to produce DNA probes useful in diagnostic assays
XX
XX
SQ

Query Match 100.0%; Score 699; DB 2; Length 1197;
Best Local Similarity 100.0%; Pred. No. 7.1e-200;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGATAGATATTTAAAGGAGAG 60
Db 181 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGATAGATATTTAAAGGAGAG 240
QY 61 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAAGTCCACCAAAATGTTTC 120
Db 241 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAAGTCCACCAAAATGTTTC 300
QY 121 CACAATGGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGTCGATGCCAAATTT 180
Db 301 CACAATGGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGTCGATGCCAAATTT 360
QY 181 GAGACAGTGGAGATCAAAATGTCAGCAACCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Db 361 GAGACAGTGGAGATCAAAATGTCAGCAACCAACAGTTAATGAGAGTGAACCTGTGTAC 420
QY 241 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGCCTCTCTGAGGTGTTGATGGAGGC 300
Db 421 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGCCTCTCTGAGGTGTTGATGGAGGC 480
QY 301 CAGCCCTCTTCTCAGTCCCATGTTGGAGCACTGGATGTGACAGAGTGAATCTAT 360
Db 481 CAGCCCTCTTCTCAGTCCCATGTTGGAGCACTGGATGTGACAGAGTGAATCTAT 540
QY 361 TATAAGCATGTTGAAGTCTCAAGTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 420
Db 541 TATAAGCATGTTGAAGTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 600
QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTCAGGCGCAAGTGTGGAGCTGGACTAT 480
Db 601 GCCACAGTTGAAGCAGTGGAACTTACTGTCAGGCGCAAGTGTGGAGCTGGACTAT 660
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGGTGAGAACTACTGGCTACAA 540
Db 661 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGGTGAGAACTACTGGCTACAA 720
QY 541 TTTTATPCCCATGTTGGTGGTGAATCTGTTTCTGTGGACACAGATTTATTTATCTCA 600
Db 721 TTTTATPCCCATGTTGGTGGTGAATCTGTTTCTGTGGACACAGATTTATTTATCTCA 780
QY 601 ACTGAGCAGAGTGCATATTTCTTGAAGTAAAGAGAACCCAGGAAGGCTTCAGACTT 660
Db 781 ACTGAGCAGAGTGCATATTTCTTGAAGTAAAGAGAACCCAGGAAGGCTTCAGACTT 840
QY 661 CTGAACCCACATCTTAAAGCCAAACCCCAAAACCAACTGA 699
Db 841 CTGAACCCACATCTTAAAGCCAAACCCCAAAACCAACTGA 879

RESULT 6
AAV36343
ID AAV36343 standard; cDNA; 1198 BP.
XX
AC AAV36343;
XX
DT 07-OCT-1998 (first entry)

XX cDNA encoding the alpha chain of a Fc epsilon receptor.
DE
XX Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
XX immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW flea allergy; heartworm infection; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT 107..880
FT CDS /*tag= a
XX
XX WO9823964-A1.
PN 04-JUN-1998.
XX
XX 24-NOV-1997; 97WO-US021651.
XX
XX 26-NOV-1996; 96US-00756387.
XX
XX (HESK-) HESKA CORP.
XX
XX Frank RG, Porter JP, Rushlow KE, Wassom DL;
XX
XX WPI: 1998-322873/28.
DR P-PSDB; AAW61190.
XX
XX Detection of non-human immunoglobulin E - by complex formation with human
XX Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
XX disease.
XX
XX Claim 11; Page 36-37; 70pp; English.
XX
XX The present sequence encodes the alpha chain of the human Fc epsilon
XX receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
XX comprises reacting isolated human Fc epsilon receptor with the test
XX sample and detecting formation of a IgE-receptor complex. Detection of
XX IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
XX internal parasitic infections or B cell neoplasia, and for measuring
XX effect of treatments. Most particularly flea allergy in dogs and cats is
XX detected, and also heartworm infection
XX
XX Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 699; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 7.1e-200;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGATAGATATTTAAAGGAGAG 60
Db 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGATAGATATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAAGTCCACCAAAATGTTTC 120
Db 242 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAAGTCCACCAAAATGTTTC 301
QY 121 CACAATGGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT 180
Db 302 CACAATGGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCCAAATTT 361
QY 181 GAAGACAGTGGAGATACAAATGTCAGCAACCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAAGACAGTGGAGATACAAATGTCAGCAACCAACAGTTAATGAGAGTGAACCTGTGTAC 421
QY 241 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGCCTCTCTGAGGTGTTGATGGAGGC 300
Db 422 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGCCTCTCTGAGGTGTTGATGGAGGC 481
QY 301 CAGCCCTCTTCTCAGTCCCATGTTGGAGCACTGGATGTGACAGAGTGAATCTAT 360
Db 482 CAGCCCTCTTCTCAGTCCCATGTTGGAGCACTGGAGTGTGTACAGGTGAATCTAT 541

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAAATCTCCATACAAAT 420
 Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAAATCTCCATACAAAT 601
 QY 421 GCCACAGTTGAGACAGTGGACCTACTACTGTAGGGGCAAGTGTGCAGCTGACTAT 480
 Db 602 GCCACAGTTGAGACAGTGGACCTACTACTGTAGGGGCAAGTGTGCAGCTGACTAT 661
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTCAA 540
 Db 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTCAA 721
 QY 541 TTTTATATCCCATTTGTTGGTGTGATCTGTTTGTGTGGACACAGGATTTATCTCA 600
 Db 722 TTTTATATCCCATTTGTTGGTGTGATCTGTTTGTGTGGACACAGGATTTATCTCA 781
 QY 601 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAAAGAACCCAGGAGGCTTCAGACTT 660
 Db 782 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAAAGAACCCAGGAGGCTTCAGACTT 841
 QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTCA 699
 Db 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTCA 880

RESULT 7

AAA34813

ID AAA34813 standard; DNA; 1198 BP.

XX AC

XX AAA34813;

 XX 28-JUL-2000 (first entry)
 DT XX
 DE XX

Human adenosine receptor related polynucleotide SEQ ID NO:2502.

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS XX

XX WO200009525-A2.

FN XX

XX 24-FEB-2000.

XX PD

XX 03-AUG-1999; 99WO-US017712.

PF XX

XX 03-AUG-1998; 98US-0095212P.

PR XX

XX (UVEC-) UNIV EAST CAROLINA.

PA XX

XX Nyce JW;

XX WPI; 2000-205971/18.

DR XX

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension,

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers.

PT PT

XX Disclosure; Page 655; 1343pp; English.

XX PS

XX The present invention describes a new composition comprising an antisense

CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have anti-inflammatory, antiallergic,

CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992), are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX

SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 3; Length 1198;

Best Local Similarity 100.0%; Pred. No. 7.1e-200; Mismatches 0; Gaps 0;

Matches 699; Conservative 0; Indels 0;

 QY 1 GTCCCTCAGAAACCTAAGGTCTCTTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
 Db 182 GTCCCTCAGAAACCTAAGGTCTCTTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 241

 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGGTTC 120
 Db 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGGTTC 301

 QY 121 CACAATGGCAGCGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180
 Db 302 CACAATGGCAGCGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 361

 QY 181 GAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
 Db 362 GAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 421

 QY 241 CTGGAAGTCTTCAGTGACTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGATGAGGGC 300
 Db 422 CTGGAAGTCTTCAGTGACTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGTGATGAGGGC 481

 QY 301 CAGCCCTCTTCCCTCAGTGGCAATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360
 Db 482 CAGCCCTCTTCCCTCAGTGGCAATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 541

 QY 361 TATAGGATGGTGAAGCTCTCAAGTACTGTATGAGACCAACCAATCTCCATACAAAT 420
 Db 542 TATAGGATGGTGAAGCTCTCAAGTACTGTATGAGACCAACCAATCTCCATACAAAT 601

 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTTACTAGGGGCAAAAGTGTGGCAGCTGACTAT 480
 Db 602 GCCACAGTTGAAGACAGTGGAACTTACTTACTAGGGGCAAAAGTGTGGCAGCTGACTAT 661

 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTCAA 540
 Db 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTCAA 721

 QY 541 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTGGACACAGGATTTATCTCA 600
 Db 722 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTGGACACAGGATTTATCTCA 781

 QY 601 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAAAGAACCCAGGAGGCTTCAGACTT 660
 Db 782 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAAAGAACCCAGGAGGCTTCAGACTT 841

QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTCA 699

Db 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 8
AAF20935
ID AAF20935 standard; DNA; 1198 BP.
XX AC AAF20935;
XX DT 14-MAR-2001 (first entry)
XX DE Human high affinity IgE receptor polynucleotide fragment #2502.
XX KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX OS Homo sapiens.
XX PN WO200062736-A2.
XX PD 26-OCT-2000.
XX PF 24-MAR-2000; 2000WO-US008020.
XX PR 06-APR-1999; 99US-0127958P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PE (NYCE/) NYCE J W.
XX PI Nyce JW;
XX DR WPI; 2000-679539/66.
XX PT Low adenosine (A) content antisense oligonucleotides which do not trigger
XX adenosine receptors during metabolism, useful e.g. for treating cancers
XX and respiratory obstructions.
XX PS Disclosure; Page 139; 1592pp; English.
XX CC The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX receptors, CNS and peripheral nervous and non-nervous system peptide
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies) or
XX surfactant hypoproduction which are associated with a disease or
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
Query Match 100.0%; Score 699; DB 3; Length 1198;
Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;
Matches 699; Conservative 0; Mismatches 0
QY 1 GTCCTCAGAAACCTTAAGTCTCTTGAACTCCCTCCAGTGAATAGATATTAAAGGAGAG 60
Db 182 GTCCTCAGAAACCTTAAGTCTCTTGAACTCCCTCCAGTGAATAGATATTAAAGGAGAG 241
QY 61 AATGAGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db 242 AATGAGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 301
QY 121 CACATGCGACGCTTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180
Db 302 CACATGCGACGCTTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 361
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421
QY 241 CTGGAAGTCTTCAGTCACTGCTGCTCTTCAGGCTCTGCTGAGTGGTGTGATGGAGGC 300
Db 422 CTGGAAGTCTTCAGTCACTGCTGCTCTTCAGGCTCTGCTGAGTGGTGTGATGGAGGC 481
QY 301 CAGCCCCCTCTCTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360
Db 482 CAGCCCCCTCTCTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTAACAAT 420
Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTAACAAT 601
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGCAGCTGGACTAT 480
Db 602 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGCAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCCCTCAACATTAATGTAATAAAGTCCGCGTGAGAACTGCGGTACAA 540
Db 662 GAGTCTGAGCCCCCTCAACATTAATGTAATAAAGTCCGCGTGAGAACTGCGGTACAA 721
QY 541 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTTGGACACAGGATTATTTATCTCA 600
Db 722 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTTGGACACAGGATTATTTATCTCA 781
QY 601 ACTCAGCAGCAGGTCACTTTCTTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 660
Db 782 ACTCAGCAGCAGGTCACTTTCTTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 841
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 699
Db 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 9
AAF77692
ID AAF77692 standard; cDNA; 1198 BP.
XX AC AAF77692;
XX DT 29-MAY-2001 (first entry)
XX DE Human wild-type FeepsilonRIalpha chain coding sequence.
XX KW Human; FeepsilonRIbeta chain; immunoglobulin E; allergy; atopy;
XX conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.
XX OS Homo sapiens.

XX WO200121816-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025877.
 XX 21-SEP-1999; 99US-0154924P.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;
 XX WPI; 2001-266077/27.
 XX Inhibiting expression of high affinity receptors for immunoglobulin (Ig) E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by contacting cell or administering to subject, a FcεR1β chain variant.
 XX Disclosure; Page 52; 55pp; English.
 XX The present invention describes a method of inhibiting the expression of the FcεsilonR1 receptor by contacting a cell expressing it with an FcεsilonR1β chain variant. The Fcεsilon receptor is a high affinity receptor for immunoglobulin E. The method is useful in the treatment of allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis, urticaria and angioedema. The present sequence is the wild-type human FcεsilonR1α chain coding sequence
 XX
 SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
 Query Match 100.0%; Score 699; DB 4; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGATAGAAATATTTAAAGGAGAG 60
 DB 182 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGATAGAAATATTTAAAGGAGAG 241
 QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGCTTC 120
 DB 242 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGCTTC 301
 QY 121 CACAATGCCAGCCCTTCAGAGAGACAAATTCAAAGTTTGAATATTTGCAATGCCAAATTT 180
 DB 302 CACAATGCCAGCCCTTCAGAGAGACAAATTCAAAGTTTGAATATTTGCAATGCCAAATTT 361
 QY 181 GAAGCAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGTGAACCTGTGTAC 240
 DB 362 GAAGCAGTGGAGATACAAATGTGAGACCAACCAAGTTAATGAGTGAACCTGTGTAC 421
 QY 241 CTGGAAGTCTTCAGTGAAGTCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGGAGGGC 300
 DB 422 CTGGAAGTCTTCAGTGAAGTCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGGAGGGC 481
 QY 301 CAGCCCTCTCTTCAGTGGCCATGTTGGAGGAACCTGGGATGTGTACAAAGTGTAT 360
 DB 482 CAGCCCTCTCTTCAGTGGCCATGTTGGAGGAACCTGGGATGTGTACAAAGTGTAT 541
 QY 361 TATAAGATGTGTGAAGTCTTCAAGTCTGTTATGAGAACCAACATCTCCATTACAAAT 420
 DB 542 TATAAGATGTGTGAAGTCTTCAAGTCTGTTATGAGAACCAACATCTCCATTACAAAT 601
 QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTACTGACGGGCAAGTGTGGCAGCTGGACTAT 480
 DB 602 GCCACAGTTGAAGCAGTGGAACTTACTGTACTGACGGGCAAGTGTGGCAGCTGGACTAT 661
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGGTGGAGTACTGGCTACAA 540
 DB 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGGTGGAGTACTGGCTACAA 721
 QY 541 TTTTATCCCAATTTGGTGGTGAATCTCTTTGCTGTGACACAGGATTTATTTATCTCA 600

DB 722 TTTTATCCCAATTTGGTGGTGAATCTCTTTGCTGTGACACAGGATTTATTTATCTCA 781
 QY 601 ACTCAGCAGCAGGTTCACATTTCTTCTTGAAGATTAAAGAACAGGAAAGCTTCAGACTT 660
 DB 782 ACTCAGCAGCAGGTTCACATTTCTTCTTGAAGATTAAAGAACAGGAAAGCTTCAGACTT 841
 QY 661 CTGAACCCCATCTCTAAGCCAAACCCCAAAACAACTGA 699
 DB 842 CTGAACCCCATCTCTAAGCCAAACCCCAAAACAACTGA 880
 XX
 RESULT 10
 AAF24912/c
 ID AAF24912 standard; DNA; 1198 BP.
 XX
 AC AAF24912;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Complement sequence of a human Fc epsilon receptor alpha-chain gene.
 XX
 KW Fc epsilon receptor; FcεsilonR; immunoglobulin E; IgE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IgE syndrome;
 KW internal parasite infection; B cell neoplasia; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104310-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-US019070.
 XX
 PR 13-JUL-1999; 99US-0143612P.
 PR 02-MAR-2000; 2000US-0186412P.
 XX
 PA (HESK-) HESKA CORP.
 PA (PROM-) PROMEGA CORP.
 XX
 PI Weber ER, Wood KV, Hall MP;
 XX
 DR WPI; 2001-103082/11.
 XX
 PT A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 XX
 PS Example; Page 61; 105pp; English.
 XX
 CC The present sequence represents the complement of a human Fc epsilon
 CC receptor (FcεsilonR) alpha-chain protein, that binds to immunoglobulin
 CC (Ig) E. The FcεsilonR domain is used to produce a fusion protein, which
 CC also comprises a luminescence inducing protein domain that induces a
 CC substrate to emit light when contacted with the luminescence inducing
 CC protein domain. The fusion protein may be used to detect IgE. It may also
 CC be used to identify a compound capable of inhibiting FcεsilonR protein
 CC activity. IgE antibody production is indicative of diseases such as
 CC allergies, atopic disease, hyper IgE syndrome, internal parasite
 CC infections and B cell neoplasia. Detection of IgE production in an animal
 CC following therapy is indicative of the efficacy of the treatment, for
 CC example when using treatments intended to disrupt IgE production
 XX
 SQ Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;
 Query Match 100.0%; Score 699; DB 5; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGATAGAAATATTTAAAGGAGAG 60
 DB 1017 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGATAGAAATATTTAAAGGAGAG 958

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
XX
Db 957 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 898
QY 121 CACAAATGGAGCCTTTACAGAGAGAGAAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180
Db 897 CACAATGGAGCCTTTACAGAGAGAGAAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 838
QY 181 GAAGACAGTGGAGAGATACAAAATGTTCAGACCAACCAAGTTTAATCAGAGTGAACCTGTGTAC 240
Db 837 GAAGACAGTGGAGAGATACAAAATGTTCAGACCAACCAAGTTTAATCAGAGTGAACCTGTGTAC 778
QY 241 CTGGAAGTCTTACAGTGAAGTCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGGC 300
Db 777 CTGGAAGTCTTACAGTGAAGTCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGGC 718
QY 301 CAGCCCTCTTCTCAGGTCGCATGTTGGAGAACTGGATGTGTACAAAGTGTATCTAT 360
Db 717 CAGCCCTCTTCTCAGGTCGCATGTTGGAGAACTGGATGTGTACAAAGTGTATCTAT 658
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTTACAAAT 420
Db 657 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTTACAAAT 598
QY 421 GCCACAGTTGAAGACAGTGGACCTACTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 540
Db 597 GCCACAGTTGAAGACAGTGGACCTACTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 538
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 478
Db 537 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 540
QY 541 TTTTATCCATGTTGGTGGTATCTGTTGGTGGACACAGGATTTTATCTCA 600
Db 477 TTTTATCCATGTTGGTGGTATCTGTTGGTGGACACAGGATTTTATCTCA 418
QY 601 ACTCAGCAGCAGTCACTTTCTTTGAAGATTAAGAACCAAGGAAAGCTTCAGCTT 660
Db 417 ACTCAGCAGCAGTCACTTTCTTTGAAGATTAAGAACCAAGGAAAGCTTCAGCTT 358
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 357 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 319

RESULT 11
AAF24911
ID AAF24911 standard; DNA; 1198 BP.
XX
AC AAF24911;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human Fc epsilon receptor alpha-chain.
XX
KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; SS.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 107..880
FT CDS
FT /*tag= a
FT /product= "Fc epsilon receptor alpha-chain"
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX

PR 13-JUL-1999; 99US-0143612P.
XX 02-MAR-2000; 2000US-0186412P.
PA (HESK-) HESKA CORP.
XX (PROM-) PROMEGA CORP.
XX Weber ER, Wood KV, Hall MP;
XX WPI; 2001-103082/11.
DR P-PSDB; AAB31584.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Claim 17; Page 58-59; 105pp; English.
XX
CC The present sequence encodes a human Fc epsilon receptor (Fc epsilonR)
CC alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilonR
CC domain is used to produce a fusion protein, which also comprises a
CC domain inducing protein domain that induces a substrate to emit
CC luminescence inducing protein domain. The fusion protein may be used to identify
CC a compound capable of inhibiting Fc epsilonR protein activity. IgE
CC antibody production is indicative of diseases such as allergies, atopic
CC disease, hyper IgE syndrome, internal parasite infections and B cell
CC neoplasia. Detection of IgE production in an animal following therapy is
CC indicative of the efficacy of the treatment, for example when using
CC treatments intended to disrupt IgE production
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;
Query Match 100.0%; Score 699; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;
Matches 699; Conservative 0; Mismatches 0;
QY 1 GTCCTCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTTAAAGGAGAG 60
Db 182 GTCCTCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATTTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTTGAATGCCAAATTT 180
Db 302 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTTGAATGCCAAATTT 361
QY 181 GAAGACAGTGGAGAGATACAAATGTTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAAGACAGTGGAGAGATACAAATGTTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 421
QY 241 CTGGAAGTCTTCAAGTGAAGTCTCTCTTCAAGGCTCTCTGAGGTCGTGATGGAGGC 300
Db 422 CTGGAAGTCTTCAAGTGAAGTCTCTCTTCAAGGCTCTCTGAGGTCGTGATGGAGGC 481
QY 301 CAGCCCTCTTCTCAGGTCGCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360
Db 482 CAGCCCTCTTCTCAGGTCGCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGACCAACATCTCCATTTACAAAT 420
Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGACCAACATCTCCATTTACAAAT 601
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTTCTGAGGCAAGTGTGGCAGCTGGACTAT 480
Db 602 GCCACAGTTGAAGACAGTGGAACTTACTTCTGAGGCAAGTGTGGCAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 540
Db 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCGTGAAGTACTGGCTACAA 721

QY 541 TTTTATCCCATCTTGGTGGTATCTGTTTCTGTGGACACAGGATTATTTATCTCA 600
 Db |||||
 722 TTTTATCCCATCTTGGTGGTATCTGTTTCTGTGGACACAGGATTATTTATCTCA 781
 QY 601 ACTGACGACGAGTGCATCTTCTTGAAGATTAAAGAGAACCCAGGAAGGCTTCAGACTT 660
 Db |||||
 782 ACTGACGACGAGTGCATCTTCTTGAAGATTAAAGAGAACCCAGGAAGGCTTCAGACTT 841
 QY 661 CTGACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 699
 Db |||||
 842 CTGACCCACATCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 12

ABL67793
 ID ABL67793 standard; DNA; 1198 BP.
 XX
 AC ABL67793;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:6130.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-US010838.
 XX

05-JUN-2000; 2000US-0209473P.
 PR 05-JUN-2000; 2000US-0209531P.
 PR 18-SEP-2000; 2000US-0233133P.
 PR 18-SEP-2000; 2000US-0233617P.
 PR 20-SEP-2000; 2000US-0234009P.
 PR 20-SEP-2000; 2000US-0234034P.
 PR 20-SEP-2000; 2000US-0234052P.
 PR 22-SEP-2000; 2000US-0234509P.
 PR 22-SEP-2000; 2000US-0234567P.
 PR 25-SEP-2000; 2000US-0234923P.
 PR 25-SEP-2000; 2000US-0234924P.
 PR 25-SEP-2000; 2000US-0235077P.
 PR 25-SEP-2000; 2000US-0235082P.
 PR 25-SEP-2000; 2000US-0235134P.
 PR 25-SEP-2000; 2000US-0235280P.
 PR 26-SEP-2000; 2000US-0235637P.
 PR 27-SEP-2000; 2000US-0235638P.
 PR 27-SEP-2000; 2000US-0235711P.
 PR 27-SEP-2000; 2000US-0235720P.
 PR 27-SEP-2000; 2000US-0235840P.
 PR 28-SEP-2000; 2000US-0235863P.
 PR 28-SEP-2000; 2000US-0236028P.
 PR 28-SEP-2000; 2000US-0236032P.
 PR 28-SEP-2000; 2000US-0236033P.
 PR 28-SEP-2000; 2000US-0236034P.
 PR 28-SEP-2000; 2000US-0236109P.
 PR 28-SEP-2000; 2000US-0236111P.
 PR 29-SEP-2000; 2000US-0236842P.
 PR 29-SEP-2000; 2000US-0236891P.
 PR 02-OCT-2000; 2000US-0237172P.
 PR 02-OCT-2000; 2000US-0237173P.
 PR 02-OCT-2000; 2000US-0237278P.
 PR 02-OCT-2000; 2000US-0237294P.
 PR 02-OCT-2000; 2000US-0237295P.
 PR 02-OCT-2000; 2000US-0237316P.
 PR 03-OCT-2000; 2000US-0237425P.
 PR 03-OCT-2000; 2000US-0237598P.

PR 03-OCT-2000; 2000US-0237604P.
 PR 03-OCT-2000; 2000US-0237606P.
 PR 03-OCT-2000; 2000US-0237608P.
 PR 01-NOV-2000; 2000US-0244867P.
 PR 01-NOV-2000; 2000US-0245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 PI
 XX WPI; 2002-188264/24.
 DR
 XX
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 XX Claim 1; SEQ ID NO 6130; 44pp; English.

CC The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
 CC tumour
 XX
 XX Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 6; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATAATTTAAAGGAGAG 60
 Db |||||
 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATAATTTAAAGGAGAG 241
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
 Db |||||
 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 301
 QY 121 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTGTGATATTTGCAATGCCAAATTT 180
 Db |||||
 302 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTGTGATATTTGCAATGCCAAATTT 361
 QY 181 GAAGACAGTGGAGATAACAAATGTCCAGCACCACCAAGTTAATGAGATGAACCTGTGTAC 240
 Db |||||
 362 GAAGACAGTGGAGATAACAAATGTCCAGCACCACCAAGTTAATGAGATGAACCTGTGTAC 421
 QY 241 CTGGAAGTCTTTCAGTGAATGCTCTCTTTCAGGCCCTCTGCTGAGGTGGTGTATGAGGGC 300
 Db |||||
 422 CTGGAAGTCTTTCAGTGAATGCTCTCTTTCAGGCCCTCTGCTGAGGTGGTGTATGAGGGC 481
 QY 301 CAGCCCTCTTCTCCCTCAGTGGCCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 360
 Db |||||
 482 CAGCCCTCTTCTCCCTCAGTGGCCATGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 541
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACACATCTCCATTACAAAT 420
 Db |||||
 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACACATCTCCATTACAAAT 601
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGCGAGCTGGACTAT 480
 Db |||||

Db 602 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 661
Qy 481 GAGCTGAGCCCTCAACATTACTGTATAAAGCTCCGGTCGAGAGTACTGGTACAA 540
Db 662 GAGCTGAGCCCTCAACATTACTGTATAAAGCTCCGGTCGAGAGTACTGGTACAA 721
Qy 541 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 600
Db 722 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 781
Qy 601 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACAGGAAAGCTTCAGACTT 660
Db 782 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACAGGAAAGCTTCAGACTT 841
Qy 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 842 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 13

ID ABZ96629

XX ABZ96629 standard; DNA; 1198 BP.

XX AC ABZ96629;

XX DT 17-OCT-2003 (first entry)

XX DE Human high affinity IgE receptor oligonucleotide fragment.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIC-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX PT ubiquinone.

XX PS Disclosure; SEQ ID NO 11871; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX CC junctions of genes encoding a polypeptide associated with lung and/or

XX CC nasal airway dysfunction and a second active agent comprising an

XX CC antiinflammatory steroid and ubiquinone. A composition of the invention

XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX CC immunosuppressive, and cytostatic activity. The composition may have a

XX CC use in antisense gene therapy. The composition is useful for treating or

XX CC preventing a respiratory, lung or malignant disease or condition, also

XX CC for enhancing the prophylactic or therapeutic respiratory effect of an

XX CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: the sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query March 100.0%; Score 699; DB 7; Length 1198;

Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;

Matches 699; Conservative 0; Mismatches 0;

Qy 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCATGGAATAGATATTAAAGGAGAG 60

Db 182 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCATGGAATAGATATTAAAGGAGAG 241

Qy 61 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCACCAATGCTTC 120

Db 242 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCACCAATGCTTC 301

Qy 121 CACAATGGCAGCCCTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCTTC 180

Db 302 CACAATGGCAGCCCTTTCAGAAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCTTC 361

Qy 181 GAACACAGTGGAGAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Db 362 GAACACAGTGGAGAATACAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421

Qy 241 CTGGAAGTCCTCAGTCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 300

Db 422 CTGGAAGTCCTCAGTCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 481

Qy 301 CAGCCCTCTTCTCCTCAGTCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 360

Db 482 CAGCCCTCTTCTCCTCAGTCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 541

Qy 361 TATAAGGATGTGAGCTCTCAAGTCTGATGATGAGACCAACACATCTCCATTACAAAT 420

Db 542 TATAAGGATGTGAGCTCTCAAGTCTGATGATGAGACCAACACATCTCCATTACAAAT 601

Qy 421 GCCACAGTTGAAGACAGTGAACCTCTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480

Db 602 GCCACAGTTGAAGACAGTGAACCTCTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 661

Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGGTGAAGAGTACTGGCTACAA 540

Db 662 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGGTGAAGAGTACTGGCTACAA 721

Qy 541 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 600

Db 722 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 781

Qy 601 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACAGGAAAGCTTCAGACTT 660

Db 782 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACAGGAAAGCTTCAGACTT 841

Qy 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699

Db 842 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 14

ADB85535

ID ADB85535 standard; cDNA; 1198 BP.

XX AC ADB85535;

XX DT 04-DEC-2003 (first entry)

XX DE Human immunoglobulin E high affinity receptor (FcERI) alpha subunit cDNA.

XX XX

PT cancers.
XX PS Disclosure; Page 658-664; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

Search completed: October 8, 2004, 23:17:39
Job time : 340.879 secs

Query Match 100.0%; Score 699; DB 3; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.1e-199;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60
DB 8534 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 8593
QY 61 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCCACCAATCGTTTC 120
DB 8594 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCCACCAATCGTTTC 8653
QY 121 CACAATGGCAGCCCTTTGAGAGAGAGACAATTCAGTTTGAATTTGTAATGCGCAATTT 180
DB 8654 CACAATGGCAGCCCTTTGAGAGAGAGACAATTCAGTTTGAATTTGTAATGCGCAATTT 8713
QY 181 GAACACAGTGGAGATACAAATGTCAGCCCAACCAAGTTAATCAGAGTGAACCTGTGTAC 240
DB 8714 GAACACAGTGGAGATACAAATGTCAGCCCAACCAAGTTAATCAGAGTGAACCTGTGTAC 8773
QY 241 CTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGAATGGAGGGC 300
DB 8774 CTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAGGTGGTGAATGGAGGGC 8833
QY 301 CAGCCCTCTTCTCAGGTGCCATGTTGAGGAACTGGGATGTTACAGGTGATCTAT 360
DB 8834 CAGCCCTCTTCTCAGGTGCCATGTTGAGGAACTGGGATGTTACAGGTGATCTAT 8893
QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGCTATGAGAACCAACATCTCCATTACAAAT 420
DB 8894 TATAAGGATGGTGAAGTCTCAAGTACTGCTATGAGAACCAACATCTCCATTACAAAT 8953
QY 421 GCCACAGTTGAAGACAGTGAAGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
DB 8954 GCCACAGTTGAAGACAGTGAAGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 9013
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCCGCGTGAGAGTACTGGCTACAA 540
DB 9014 GAGTCTGAGCCCTCAACATTTACTGTATTAAGCTCCGCGTGAGAGTACTGGCTACAA 9073
QY 541 TTTTATATCCCATTTGTTGGTGGTCAATTCGTTTCTGTGGACACAGGATTTATTATCTCA 600

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	699	100.0	699	2	US-08-756-387B-7
2	699	100.0	699	4	US-09-285-873-7
3	699	100.0	699	4	US-09-944-277A-7
4	699	100.0	774	2	US-08-756-387B-4
5	699	100.0	774	2	US-08-756-387B-5
6	699	100.0	774	4	US-09-285-873-4
7	699	100.0	774	4	US-09-285-873-5
8	699	100.0	774	4	US-09-944-277A-4
9	699	100.0	774	4	US-09-944-277A-5
10	699	100.0	1174	1	US-07-869-933-10
11	699	100.0	1174	3	US-09-103-663-10
12	699	100.0	1198	2	US-08-756-387B-1
13	699	100.0	1198	2	US-08-756-387B-3
14	699	100.0	1198	4	US-09-285-873-1
15	699	100.0	1198	4	US-09-285-873-3
16	699	100.0	1198	4	US-09-944-277A-1
17	699	100.0	1198	4	US-09-944-277A-3
18	698	99.9	773	4	US-08-897-556A-6
19	537.8	76.9	2955	4	US-08-897-556A-4
20	516	73.8	516	2	US-08-756-387B-12
21	516	73.8	516	4	US-09-285-873-12
22	516	73.8	516	4	US-09-944-277A-12
23	516	73.8	591	2	US-08-756-387B-10
24	516	73.8	591	4	US-09-285-873-10
25	516	73.8	591	4	US-09-944-277A-10
26	516	73.8	713	2	US-08-238-027-3
27	514.4	73.6	591	3	US-08-788-954-1

28	395.8	56.6	1015	3	US-09-015-734-1	Sequence 1, Appli
c 29	395.8	56.6	1015	3	US-09-015-734-3	Sequence 3, Appli
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c 31	395.8	56.6	1015	4	US-09-515-311-3	Sequence 3, Appli
32	392.4	56.1	708	3	US-09-015-734-6	Sequence 6, Appli
c 33	392.4	56.1	708	3	US-09-015-734-8	Sequence 8, Appli
34	392.4	56.1	708	4	US-09-515-311-6	Sequence 6, Appli
c 35	392.4	56.1	708	4	US-09-515-311-8	Sequence 8, Appli
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c 37	392.4	56.1	765	3	US-09-015-734-5	Sequence 5, Appli
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c 39	392.4	56.1	765	4	US-09-515-311-5	Sequence 5, Appli
40	376.4	53.8	1069	2	US-08-768-964-1	Sequence 1, Appli
c 41	376.4	53.8	1069	2	US-08-768-964-3	Sequence 3, Appli
42	376.4	53.8	1069	3	US-09-005-299-1	Sequence 1, Appli
c 43	376.4	53.8	1069	3	US-09-005-299-3	Sequence 3, Appli
44	376.4	53.8	1069	3	US-09-515-431-1	Sequence 1, Appli
c 45	376.4	53.8	1069	3	US-09-515-431-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
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; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
US-08-756-387B-7

Query Match 100.0%; Score 699; DB 2; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.5e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCCCTCAGAAACCTTAAGTCTTCCTTGAACCCCTCATGAAATAGAAATATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAAACCTTAAGTCTTCCTTGAACCCCTCATGAAATAGAAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120

QY 121 CACAATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180

QY 181 GAAGACAGTGGAGATACAAATGTGAGCAACAACAGTTAATGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGATACAAATGTGAGCAACAACAGTTAATGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 300
Db 241 CTGGAAGTCTTTCAGTGAAGTCTCTCCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGGCATGGTTGGAGGAACCTGGGATGTGTAAGGTGATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGGCATGGTTGGAGGAACCTGGGATGTGTAAGGTGATCTAT 360

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGAGCAACAACATCTCCATTACAAAT 420
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGAGCAACAACATCTCCATTACAAAT 420

QY 421 GCCCAGTGAAGACAGTGAACCTTACTGATGTAAGATTAAGAGACCAAGTGGAGTGGACTAT 480
Db 421 GCCCAGTGAAGACAGTGAACCTTACTGATGTAAGATTAAGAGACCAAGTGGAGTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 540
Db 481 GAGTCTGAGCCCTCAACATTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 540

QY 541 TTTTATTCATTTGTTGGTGGTGAATCTGTTTCTGTTGAGCAGCAGGATTTATTTCTCA 600
Db 541 TTTTATTCATTTGTTGGTGGTGAATCTGTTTCTGTTGAGCAGCAGGATTTATTTCTCA 600

QY 601 ACTCAGCAGCAGTGAACCTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 660
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RESULT 2

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US-09-285-873-7
; Sequence 7, Application US/09285873
; Patent No. 6309832

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GENERAL INFORMATION:

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; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95

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; SOFTWARE: WordPerfect for Windows, Version 7.0

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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/285,873

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; FILING DATE:

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; CLASSIFICATION:

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/08/756,387

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; FILING DATE: NO. 6309832ember 26, 1996

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; ATTORNEY/AGENT INFORMATION:

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; NAME: Verser, Carol Talkington

```

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; REGISTRATION NUMBER: 37,459

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; REFERENCE/DOCKET NUMBER: DI-1

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; TELECOMMUNICATION INFORMATION:

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```

; TELEPHONE: 970/493-7272

```

```

; TELEFAX: 970/484-9505

```

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; INFORMATION FOR SEQ ID NO: 7:

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; SEQUENCE CHARACTERISTICS:

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; LENGTH: 699 nucleotides

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; TYPE: nucleic acid

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; STRANDEDNESS: single

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; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA

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; FEATURE:

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; NAME/KEY: CDS

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; LOCATION: 1..699

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; US-09-285-873-7

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Query Match

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Best Local Similarity 100.0%; Score 699; DB 4; Length 699;

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Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCCCTCAGAAACCTTAAGTCTTCCTTGAACCCCTCATGAAATAGAAATATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAAACCTTAAGTCTTCCTTGAACCCCTCATGAAATAGAAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120

QY 121 CACAATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180
Db 121 CACAATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180

QY 181 GAAGACAGTGGAGATACAAATGTGAGCAACAACAGTTAATGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGATACAAATGTGAGCAACAACAGTTAATGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 300
Db 241 CTGGAAGTCTTTCAGTGAAGTCTCTCCTTCAGGCTCTGCTGAGGTGGTGAAGGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGGCATGGTTGGAGGAACCTGGGATGTGTAAGGTGATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGGCATGGTTGGAGGAACCTGGGATGTGTAAGGTGATCTAT 360

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGAGCAACAACATCTCCATTACAAAT 420
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGAGCAACAACATCTCCATTACAAAT 420

QY 421 GCCCAGTGAAGACAGTGAACCTTACTGATGTAAGATTAAGAGACCAAGTGGAGTGGACTAT 480
Db 421 GCCCAGTGAAGACAGTGAACCTTACTGATGTAAGATTAAGAGACCAAGTGGAGTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 540
Db 481 GAGTCTGAGCCCTCAACATTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 540

QY 541 TTTTATTCATTTGTTGGTGGTGAATCTGTTTCTGTTGAGCAGCAGGATTTATTTCTCA 600
Db 541 TTTTATTCATTTGTTGGTGGTGAATCTGTTTCTGTTGAGCAGCAGGATTTATTTCTCA 600

QY 601 ACTCAGCAGCAGTGAACCTTCTTGAAGTCTGTAAGTCTGGGATGTAAGTCTGGTACTCA 660

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Db 601 ACTCAGCAGCGTCACTTTCTTGAAGATTAAAGAACACGAAAGGCTTACAGACTT 660
QY 661 CTGAACCCCACTCTTAAGCCAAACCCCAAACTGA 699
Db 661 CTGAACCCCACTCTTAAGCCAAACCCCAAACTGA 699

RESULT 3
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

Query Match 100.0%; Score 699; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.5e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60
Db 1 GTCCTCAGAAACCTAAGGTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60

QY 61 AATGTGACTCTTACATGATGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120
Db 61 AATGTGACTCTTACATGATGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120

QY 121 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAAAATTT 180
Db 121 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAAAATTT 180

QY 181 GAAGACAGTGGGAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGGAATACAAATGTCAGCACCAACAACTTAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTTCAGTGTCTGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTATGGAGGC 300
Db 241 CTGGAAGTCTTTCAGTGTCTGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTATGGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGTCTGCTCTGAGGAGTGGGATGTTGTAAGGTTGATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGTCTGCTCTGAGGAGTGGGATGTTGTAAGGTTGATCTAT 360

QY 361 TATAAGGATGTTGAAGTCTCAAGTACTGTTGATGAGAACCAACATCTCCATTACAAAT 420
Db 361 TATAAGGATGTTGAAGTCTCAAGTACTGTTGATGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTTAGGGGAAAGTGTGGCAGTGGACTAT 480
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTTAGGGGAAAGTGTGGCAGTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTACTGTTAAATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 540
Db 481 GAGTCTGAGCCCTCAACATTTACTGTTAAATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 540

QY 541 TTTTATCCCATTTGTTGGTGTGATTTCTGTTGATTTCTGTTGACACAGGATTTATCTCA 600
Db 541 TTTTATCCCATTTGTTGGTGTGATTTCTGTTGATTTCTGTTGACACAGGATTTATCTCA 600

QY 601 ACTCAGCAGCGTCACTTTCTTGAAGATTAAAGAACCCAGGAAAGGCTTCAGACTT 660
Db 601 ACTCAGCAGCGTCACTTTCTTGAAGATTAAAGAACCCAGGAAAGGCTTCAGACTT 660

QY 661 CTGAACCCCACTCTTAAGCCAAACCCCAAACTGA 699
Db 661 CTGAACCCCACTCTTAAGCCAAACCCCAAACTGA 699

RESULT 4
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-08-756-387B-4

Query Match      100.0%; Score 699; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||
QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGTTTC 195
Db |||||
QY 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATATTTGTAATGCAAAATTT 180
Db |||||
QY 196 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATATTTGTAATGCAAAATTT 255
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QY 181 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db |||||
QY 256 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 315
Db |||||
QY 241 CTGGAAGTCTTCAGTGAAGTGGTCTCTCTTGAAGTCAGTTCACCAAAATGTTTC 300
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QY 316 CTGGAAGTCTTCAGTGAAGTGGTCTCTCTTGAAGTCAGTTCACCAAAATGTTTC 375
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QY 301 CAGCCCTCTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAGTGTATCTAT 360
Db |||||
QY 376 CAGCCCTCTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAGTGTATCTAT 435
Db |||||
QY 361 TATAAGGATGGTGAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT 420
Db |||||
QY 436 TATAAGGATGGTGAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT 495
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QY 421 GCCACAGTTGAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 480
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QY 496 GCCACAGTTGAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 555
Db |||||
QY 481 GAGTCTGAGCCCTCAACATTTCTGTAATTAAGTCTCCGGTGGAGAGTACTGGCTACAA 540
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QY 556 GAGTCTGAGCCCTCAACATTTCTGTAATTAAGTCTCCGGTGGAGAGTACTGGCTACAA 615
Db |||||
QY 541 TTTTATTTATCCATGTTGGTGGTGAATCTCTTGAAGTCTCCGGTGGAGAGTACTGGCTACAA 600
Db |||||
QY 616 TTTTATTTATCCATGTTGGTGGTGAATCTCTTGAAGTCTCCGGTGGAGAGTACTGGCTACAA 675
Db |||||
QY 601 ACTCAGCAGAGGTCACATTTCTTGAAGTCTCCGGTGGAGAGTACTGGCTACAA 560
Db |||||
QY 676 ACTCAGCAGAGGTCACATTTCTTGAAGTCTCCGGTGGAGAGTACTGGCTACAA 735
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QY 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACCACTGA 699
Db |||||
QY 736 CTGAACCCCATCTTAAGCCAAACCCCAAAACCACTGA 774
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RESULT 5

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US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
```

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; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-756-387B-5
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Query Match      100.0%; Score 699; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
QY 699 GTCCTCAGAAACCTAAGGCTCTCTTGAACCTCCATGGATAGAAATTTAAAGGAGAG 640
Db |||||
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGTTTC 120
Db |||||
QY 639 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGTTTC 580
Db |||||
QY 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATATTTGTAATGCAAAATTT 180
Db |||||
QY 579 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGATTTGAATATTTGTAATGCAAAATTT 520
Db |||||
QY 181 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db |||||
QY 519 GAAGACAGTGGAGAAATCAAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 460
Db |||||
QY 241 CTGGAAGTCTTCAGTGAAGTGGTCTCTCTTGAAGTCAGTTCACCAAAATGTTTC 300
Db |||||
QY 459 CTGGAAGTCTTCAGTGAAGTGGTCTCTCTTGAAGTCAGTTCACCAAAATGTTTC 400
Db |||||
QY 301 CAGCCCTCTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAGTGTATCTAT 360
Db |||||
QY 399 CAGCCCTCTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGACAGTGTATCTAT 340
Db |||||
QY 361 TATAAGGATGGTGAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT 420
Db |||||
QY 339 TATAAGGATGGTGAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGT 280
Db |||||
QY 421 GCCACAGTTGAGAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 480
Db |||||
QY 279 GCCACAGTTGAGAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 220
Db |||||
QY 481 GAGTCTGAGCCCTCAACATTTCTGTAATTAAGTCTCCGGTGGAGAGTACTGGCTACAA 540
Db |||||
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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-285-873-5

Query Match 100.0%; Score 699; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 60
DB 699 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 640

QY 61 AATGTGACTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 639 AATGTGACTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 590

QY 121 CACATGGCAGCTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 180
DB 579 CACATGGCAGCTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 520

QY 181 GAAGACAGTGGAGAAATCAAAATGTGAGAGACCAACCAAGTGAATGAGAGTGAATGATCTAT 240
DB 519 GAAGACAGTGGAGAAATCAAAATGTGAGAGACCAACCAAGTGAATGAGAGTGAATGATCTAT 460

QY 241 CTGGAAGTCTTTCAGTGTGCTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 300
DB 459 CTGGAAGTCTTTCAGTGTGCTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 400

QY 301 CAGCCCTCTTCTCAGTGTGCTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 360
DB 399 CAGCCCTCTTCTCAGTGTGCTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 340

QY 361 TATAAGGATGGTGAAGCTCTCAAGTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTAT 420
DB 339 TATAAGGATGGTGAAGCTCTCAAGTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTAT 280

QY 421 GCCACAGTGGAGACAGTGGAACTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 480
DB 279 GCCACAGTGGAGACAGTGGAACTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTCTAT 220

QY 481 GAGTCTGAGCCCTTCAACATTTCTTCAAGTGAATGAAGTCTCTTCAAGTGAATGAAGTCTAT 540
DB 219 GAGTCTGAGCCCTTCAACATTTCTTCAAGTGAATGAAGTCTCTTCAAGTGAATGAAGTCTAT 160

QY 541 TTTTATATCCATTTGTTGGTGGTATCTCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 600
DB 159 TTTTATATCCATTTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 100

QY 601 ACTCAGCAGAGGTCACATTTCTTCAAGTGAATGAAGTCTCTTCAAGTGAATGAAGTCTAT 660
DB 99 ACTCAGCAGAGGTCACATTTCTTCAAGTGAATGAAGTCTCTTCAAGTGAATGAAGTCTAT 40

QY 661 CTGAACCCCATCTTAAAGCCAAACCCCAAAACCAACTGA 699
DB 39 CTGAACCCCATCTTAAAGCCAAACCCCAAAACCAACTGA 1
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RESULT 8
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; PORTER, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4
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Query Match 100.0%; Score 699; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 60
DB 76 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 135

QY 61 AATGTGACTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB 136 AATGTGACTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195

QY 121 CACATGGCAGCTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 180
DB 196 CACATGGCAGCTTTACATGTAATGGAAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 255

QY 181 GAAGACAGTGGAGAAATCAAAATGTGAGAGACCAACCAAGTGAATGAGAGTGAATGATCTAT 240
DB 256 GAAGACAGTGGAGAAATCAAAATGTGAGAGACCAACCAAGTGAATGAGAGTGAATGATCTAT 315

QY 241 CTGGAAGTCTTTCAGTGTGCTCTCTTCAAGCTCTCTTCAAGCTCTCTTCAAGCTCTAT 300
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; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..880
; US-07-869-933-10

Query Match 100.0%; Score 699; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.1e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
DB 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 301
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 180
DB 362 GAAGACAGTGGAGAAATACAAATGTGAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 421
QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTCTGAGGCTCTCTGAGGCTCT 300
DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTCTGAGGCTCTCTGAGGCTCT 481
QY 301 CAGCCCTCTTCTCAGTGGTCCATGTTGAGGAACTGGGATGTGTAAGAGTGTAT 360
DB 482 CAGCCCTCTTCTCAGTGGTCCATGTTGAGGAACTGGGATGTGTAAGAGTGTAT 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAAT 420
DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAAT 601
QY 421 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 480
DB 602 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAAATGAAGCTCCGGTGTAGAGTACTGGCTACAA 540
DB 662 GAGTCTGAGCCCTCAACATTTACTGTAAATGAAGCTCCGGTGTAGAGTACTGGCTACAA 721
QY 541 TTTTATCCCATTTGTTGGTGTGATCTGTTGCTGTGACACAGGATTTATTTATCTCA 600

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DB 722 TTTTATCCCATTTGTTGGTGTGATCTGTTGCTGTGACACAGGATTTATTTATCTCA 781
QY 601 ACTCAGCAGCAGGTCAACATTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 660
DB 782 ACTCAGCAGCAGGTCAACATTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 841
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACCTGA 699
DB 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACCTGA 880

RESULT 11
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(880)
; US-09-103-663-10

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Query Match 100.0%; Score 699; DB 3; Length 1174;
Best Local Similarity 100.0%; Pred. No. 2.1e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
DB 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 301
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 180
DB 302 CACAATGGCAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 361
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 240
DB 362 GAAGACAGTGGAGAAATACAAATGTGAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 421
QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTCTGAGGCTCTCTGAGGCTCT 300
DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTCTGAGGCTCTCTGAGGCTCT 481
QY 301 CAGCCCTCTTCTCAGTGGTCCATGTTGAGGAACTGGGATGTGTAAGAGTGTAT 360
DB 482 CAGCCCTCTTCTCAGTGGTCCATGTTGAGGAACTGGGATGTGTAAGAGTGTAT 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAAT 420
DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACATCTCCATTACAAAT 601
QY 421 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 480
DB 602 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGTGGCAGCTGGACTAT 661

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; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-756-387B-3

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Query Match          100.0%; Score 699; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.le-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCCCTCAGAACCTTAAGCTCTCTTGAACCCCTCATGGATAGATAATTTAAAGGAGAG 60
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QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Db |||||||
QY 957 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 898
Db |||||||
QY 121 CACATGCGAGCTTTACAGAGAGACAATTTCAAGTTTGAATATTTGAATGCGCAATTT 180
Db |||||||
QY 897 CACATGCGAGCTTTACAGAGAGACAATTTCAAGTTTGAATATTTGAATGCGCAATTT 898
Db |||||||
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAGCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
Db |||||||
QY 837 GAAGACAGTGGAGAAATACAAATGTGAGCAGCAACAAGTTAATGAGAGTGAACCTGTGTAC 778
QY 241 CTGGAAGTCTTTCAGTACTGCTCTCTTTCAGGCTCTCTCTGAGGCTCTCTGAGGCTGAGGAGGC 300
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QY 777 CTGGAAGTCTTTCAGTACTGCTCTCTTTCAGGCTCTCTCTGAGGCTCTCTGAGGCTGAGGAGGC 718
QY 301 CAGCCCTCTTCTCAGTGCATGCTTGGAGGAGTGGAGTGTGACAGGAGTGTATCTAT 360
Db |||||||
QY 717 CAGCCCTCTTCTCAGTGCATGCTTGGAGGAGTGGAGTGTGACAGGAGTGTATCTAT 658
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCTCATTACAAAT 420
Db |||||||
QY 657 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCTCATTACAAAT 598
QY 421 GCCACAGTTGAGACAGTGGAGTCTTCTGAGTCTGAGGAGTGGAGTGGAGTGGAGTGGAGTAT 480
Db |||||||
QY 597 GCCACAGTTGAGACAGTGGAGTCTTCTGAGTCTGAGGAGTGGAGTGGAGTGGAGTGGAGTAT 538
QY 481 GAGTCTGAGCCCTTCAACATTTACTGTATTAATAAAGCTCCGCTGAGAGTACTGGCTACAA 540
Db |||||||
QY 537 GAGTCTGAGCCCTTCAACATTTACTGTATTAATAAAGCTCCGCTGAGAGTACTGGCTACAA 478
QY 541 TTTTATATCCATTTGTTGGTGGTGAATCTGTTGCTGTGACACAGATTTATTTATCTCA 600
Db |||||||
QY 477 TTTTATATCCATTTGTTGGTGGTGAATCTGTTGCTGTGACACAGATTTATTTATCTCA 418
QY 601 ACTCAGCAGAGGTCACATTTCTCTCAAGATTAAGAGAACCAAGGAGTGGAGTGGAGTGGAGT 660
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QY 417 ACTCAGCAGAGGTCACATTTCTCTGAGATTAAGAGAACCAAGGAGTGGAGTGGAGTGGAGT 358
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QY 357 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 319

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RESULT 14

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US-09-285-873-1
; Sequence 1, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:

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; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; US-09-285-873-1

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Query Match          100.0%; Score 699; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.le-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCATGGATAGATAATTTAAAGGAGAG 60
Db |||||||
QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Db |||||||
QY 242 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 301
QY 121 CACATGCGAGCTTTACAGAGAGACAATTTCAAGTTTGAATATTTGAATGCGCAATTT 180
Db |||||||
QY 302 CACATGCGAGCTTTACAGAGAGACAATTTCAAGTTTGAATATTTGAATGCGCAATTT 361
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db |||||||
QY 362 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421
QY 241 CTGGAAGTCTTTCAGTACTGCTCTCTTTCAGGCTCTCTCTGAGGCTCTCTGAGGCTGAGGAGGC 300
Db |||||||
QY 422 CTGGAAGTCTTTCAGTACTGCTCTCTTTCAGGCTCTCTCTGAGGCTCTCTGAGGCTGAGGAGGC 481
QY 301 CAGCCCTCTTCTCAGTGCATGCTTGGAGGAGTGGAGTGTGACAGGAGTGTATCTAT 360
Db |||||||
QY 482 CAGCCCTCTTCTCAGTGCATGCTTGGAGGAGTGGAGTGTGACAGGAGTGTATCTAT 541

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473	QY		532

RESULT 15

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US-09-285-873-3/C
; Sequence 3, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-285-873-3

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Query Match

100.0%; Score 699; DB 4; Length 1198;

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Best Local Similarity 100.0%; Pred. No. 2.1e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAATATTAAAGGAGAG 60
DB      1017 GTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAATATTAAAGGAGAG 958

QY      61  AATGTGACTCTTACATGTTAATGGGAACAATTCCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB      957  AATGTGACTCTTACATGTTAATGGGAACAATTCCTTTGAAGTCAGTTCCACCAATGGTTC 898

QY      121  CACAATGGCAGCCCTTTCAGAGAAGACAAATTCCAAGTTTGAATATTGTGAATGCCAAATTT 180
DB      897  CACAATGGCAGCCCTTTCAGAGAAGACAAATTCCAAGTTTGAATATTGTGAATGCCAAATTT 838

QY      181  GAAGACAGTGGGAATACAAATGTCAAGACCAACAAGTTAATCAGAGAGTGAACCTGTGTAC 240
DB      837  GAAGACAGTGGGAATACAAATGTCAAGACCAACAAGTTAATCAGAGAGTGAACCTGTGTAC 778

QY      241  CTGGAAGTCTTCAGTCAGCTGGCTGCTCTTCAGGCCCTCTGCTCAGGTGGTGTGATGGAGGGC 300
DB      777  CTGGAAGTCTTCAGTCAGCTGGCTGCTCTTCAGGCCCTCTGCTCAGGTGGTGTGATGGAGGGC 718

QY      301  CAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 360
DB      717  CAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTGTACAAGGTGATCTAT 658

QY      361  TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCACAACTCTCCATTACAAT 420
DB      657  TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCACAACTCTCCATTACAAT 598

QY      421  GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCCAAAGTGTGGCAGCTGGACTAT 480
DB      597  GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCCAAAGTGTGGCAGCTGGACTAT 538

QY      481  GAGTCTGAGCCCTCAACATTACTGTATAAAGACTCCGCGTGAGAGTACTGGCTACAA 540
DB      537  GAGTCTGAGCCCTCAACATTACTGTATAAAGACTCCGCGTGAGAGTACTGGCTACAA 478

QY      541  TTTTATATCCCATGTTGGTGGTGAATCTGTTTGTGTGGACACAGGATTATTTATCTCA 600
DB      477  TTTTATATCCCATGTTGGTGGTGAATCTGTTTGTGTGGACACAGGATTATTTATCTCA 418

QY      601  ACTCAGCAGAGTCAATTTCTTGTGAAGATTAAAGAAACCAGGAAGGCTTCAGACTT 660
DB      417  ACTCAGCAGAGTCAATTTCTTGTGAAGATTAAAGAAACCAGGAAGGCTTCAGACTT 358

QY      661  CTCGAACCCACATCCTAAGCCAAACCCCAAAAAACAACCTGA 699
DB      357  CTCGAACCCACATCCTAAGCCAAACCCCAAAAAACAACCTGA 319

Search completed: October 10, 2004, 11:20:18
Job time : 62.7962 secs

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Search completed: October 10, 2004, 11:20:18
Job time : 62.7962 secs

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Sequence 2037, Ap
Sequence 266, App
Sequence 244, App
Sequence 22, Appli
Sequence 1306, Ap
Sequence 286, App
Sequence 13, Appli

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18.7 1074 15 US-10-027-736A-1

ALIGNMENTS

RESULT 1
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasslow, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION NUMBER: US/09/944,277A
; APPLICATION NUMBER: 30-Aug-2001
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

15 455 65.1 757 13 US-10-236-392-29
16 395.8 56.6 1015 16 US-10-434-817-1
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20 392.4 56.1 765 16 US-10-434-817-4
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24 167 23.9 887 17 US-10-027-736A-8
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27 165.4 23.7 887 17 US-10-641-643-1254
28 165.4 23.7 887 17 US-10-717-597-208
29 165.4 23.7 887 17 US-10-775-169-140
30 165.4 23.7 2463 15 US-10-240-965-100
31 162.2 23.2 1977 10 US-09-873-367C-994
32 162.2 23.2 1977 13 US-10-342-887-382
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35 162.2 23.2 765 15 US-10-027-736A-7
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Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues
Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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3	699	100.0	774	9 US-09-944-277A-5	Sequence 5, Appli
4	699	100.0	1198	9 US-09-944-277A-1	Sequence 1, Appli
5	699	100.0	1198	9 US-09-944-277A-3	Sequence 3, Appli
6	699	100.0	1198	9 US-09-962-832-244	Sequence 244, App
7	699	100.0	1198	17 US-10-775-169-141	Sequence 141, App
8	697.4	99.8	898	13 US-10-236-392-27	Sequence 27, Appli
9	528	75.5	528	10 US-09-809-715-1	Sequence 1, Appli
10	528	75.5	528	13 US-10-293-992-1	Sequence 1, Appli
11	516	73.8	516	9 US-09-944-277A-12	Sequence 12, Appli
12	516	73.8	516	13 US-10-293-992-3	Sequence 3, Appli
13	516	73.8	591	9 US-09-944-277A-10	Sequence 10, Appli
14	515.2	73.7	528	10 US-09-809-715-3	Sequence 3, Appli

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436 TATAAGAGTGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 495
Qy 421 GCCACAGTTGAAGACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480
Db 496 GCCACAGTTGAAGACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 555
Qy 481 GAGTCTCAGCCCTCAACATTACTGTATATAAAGCTCCGGGTGAGAACTACTGGCTACAA 540
Db 556 GAGTCTCAGCCCTCAACATTACTGTATATAAAGCTCCGGGTGAGAACTACTGGCTACAA 615
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Qy 601 ACTCAGCAGAGCTCACATTCTCTGAAGATTAAAGACACCAAGAGCTTCAGACTT 660
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RESULT 3
US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

Query Match 100.0%; Score 699; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 7e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 699 GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATCGAATAGATAATTTAAAGGAGAG 640
Qy 61 AATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
Db 639 AATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 580
Qy 121 CCAATGCGAGCCCTTTCAGAGAGACAAATTCAGATTTTGAATATGTAATGCCAAATTT 180
Db 579 CCAATGCGAGCCCTTTCAGAGAGACAAATTCAGATTTTGAATATGTAATGCCAAATTT 520
Qy 181 GAAGACAGTGGAGATACAAATGTGAGCAACCAAAAGTTAATGAGAGTGAACCTGTGTAC 240
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Qy 241 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTGTATGGAGGCG 300
Db 459 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCTCTGCTGAGGTGGTGTATGGAGGCG 400
Qy 301 CAGCCCTCTTCTCAGTGGCTGCTGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360
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Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
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Db 279 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAGTGTGGAGCTGGACTAT 220
Qy 481 GAGTCTGAGCCCTCAACATTTACTCTATAAAGCTCCGCGTGAAGTACTGGGTACAA 540
Db 219 GAGTCTGAGCCCTCAACATTTACTCTATAAAGCTCCGCGTGAAGTACTGGGTACAA 160
Qy 541 TTTTATATCCATTGTTGGTGGTATCTGTTGCTGTGGACACAGGATTATTTATCTCA 600
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RESULT 4
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-1

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match      100.0%; Score 699; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 9.4e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGAAATAGAAATATTAAAGGAGAG 60
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DB 242 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGCTTC 301
QY 121 CACAATGGCAGCTTTTCAGAGAGACAAATTCAAAGTTTGAATTTGTAATGCCAAATTT 180
DB 302 CACAATGGCAGCTTTTCAGAGAGACAAATTCAAAGTTTGAATTTGTAATGCCAAATTT 361
QY 181 GAAGCAGTGGAGATACAAATGTCAGCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
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QY 241 CTGGAAGTCTTTCAGTACTGCTCTCTCAGGCCTCTCTGAGGTGGTGATGGAGGC 300
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QY 301 CAGCCCTCTCTCTCAGTGGCCATGTTGGAGGAACCTGGAGTGTGTAAGGTGATCTAT 360
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QY 421 GCCACAGTTGAAGACAGTGGACCTACTACTGTACGGGCAAGGTGGCAGCTGGACTAT 480
DB 602 GCCACAGTTGAAGACAGTGGACCTACTACTGTACGGGCAAGGTGGCAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATTAAGTCCCGGTGAGAGTACTGGCTACAA 540
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RESULT 5
US-09-944-277A-3/C
; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

Query Match      100.0%; Score 699; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 9.4e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGAAATAGAAATATTAAAGGAGAG 60
DB 1017 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGAAATAGAAATATTAAAGGAGAG 958
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DB 957 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTCCACCAATGCTTC 898
QY 121 CACAATGGCAGCTTTTCAGAGAGACAAATTCAAAGTTTGAATTTGTAATGCCAAATTT 180

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777 CTGGAAGTCTTTCAGTGAAGTGGTCTCCTTCAGGCTCTCTCTGAGTGTGTGTGAGGCG 718
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717 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 658
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657 TATAAGGATGGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 598
421 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 480
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481 GAGTCTGAGCCCTCAACATCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 540
537 GAGTCTGAGCCCTCAACATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 478
541 TTTTATCCATGTTGGTGTGATCTCTTCTGAGTGTGAGAACCAACATCTCCATTAACAAT 600
477 TTTTATCCATGTTGGTGTGATCTCTTCTGAGTGTGAGAACCAACATCTCCATTAACAAT 418
601 ACTCAGCAGCAGTCAATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 660
417 ACTCAGCAGCAGTCAATCTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 358
661 CTGAACCCACATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 699
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RESULT 6
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; Sequence 244, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-244

Query Match 100.0%; Score 699; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 9.4e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
182 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 241
61 AATGTGACTCTTACATGTATGGAACAAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 120
242 AATGTGACTCTTACATGTATGGAACAAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 301

121 CACAATGGCAGCCTTTTCAGAAAGACACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
302 CACAATGGCAGCCTTTTCAGAAAGACACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 361
181 GAAGACAGTGGGAATACAAATCTCAGCACCAACAAAGTTAAATGAGAGTCAACTGTGTAC 240
362 GAAGACAGTGGGAATACAAATCTCAGCACCAACAAAGTTAAATGAGAGTCAACTGTGTAC 421
241 CTGGAAGTCTTTCAGTGAAGTGGTCTCCTTCAGGCTCTCTCTGAGTGTGTGTGAGGCG 300
422 CTGGAAGTCTTTCAGTGAAGTGGTCTCCTTCAGGCTCTCTCTGAGTGTGTGTGAGGCG 481
301 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
482 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 541
361 TATAAGGATGGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 420
542 TATAAGGATGGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 601
421 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 480
602 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 661
481 GAGTCTGAGCCCTCAACATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 540
662 GAGTCTGAGCCCTCAACATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 721
541 TTTTATCCATGTTGGTGTGATCTCTTCTGAGTGTGAGAACCAACATCTCCATTAACAAT 600
722 TTTTATCCATGTTGGTGTGATCTCTTCTGAGTGTGAGAACCAACATCTCCATTAACAAT 781
601 ACTCAGCAGCAGTCAATCTCTTGAAGTAAAGAACCAACATCTCCATTAACAAT 660
782 ACTCAGCAGCAGTCAATCTCTTGAAGTAAAGAACCAACATCTCCATTAACAAT 841
661 CTGAACCCACATCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 699
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RESULT 7
US-10-775-169-141
; Sequence 141, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM10180 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-141

Query Match 100.0%; Score 699; DB 17; Length 1198;
Best Local Similarity 100.0%; Pred. No. 9.4e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
182 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 241
61 AATGTGACTCTTACATGTATGGAACAAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 120

Db 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGGAACCTGGATGTGTCAAGGTGATCTAT 360
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
 Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
 Qy 421 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480
 Db 421 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480
 Qy 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCTCCGCGTGAGAAG 528
 Db 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCTCCGCGTGAGAAG 528

RESULT 11

US-09-944-277A-12

; Sequence 12, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; City: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 516 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..516

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-944-277A-12

Query Match 73.8%; Score 516; DB 9; Length 516;

Best Local Similarity 100.0%; Pred. No. 5.4e-158;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAACCTAAGGTCCTCTGAACCCCTCATGGAATAGATATTAAAGGAGAG 60

Db 1 GTCCCTCAGAACCTAAGGTCCTCTGAACCCCTCATGGAATAGATATTAAAGGAGAG 60

Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
 Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
 Qy 121 CACAATGGCAGCCTTTTCAGAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180
 Db 121 CACAATGGCAGCCTTTTCAGAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180
 Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
 Db 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
 Qy 241 CTGGAAGTCTTCAGTGACTGGCTGTCTCTCAGGCTCTGTGAGGTGTGTGATGAGGGC 300
 Db 241 CTGGAAGTCTTCAGTGACTGGCTGTCTCTCAGGCTCTGTGAGGTGTGTGATGAGGGC 300
 Qy 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTGTACAAGTGAATCTAT 360
 Db 301 CAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTGTACAAGTGAATCTAT 360
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
 Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
 Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 Db 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
 Qy 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCT 516
 Db 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCT 516

RESULT 12

US-10-293-992-3

; Sequence 3, Application US/10293992

; Publication No. US20040033527A1

; GENERAL INFORMATION:

; APPLICANT: Jardtzy, Theodore S.

; APPLICANT: Garman, Scott Clayton

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR

; TITLE OF INVENTION: CHAIN

; FILE REFERENCE: AL-3-CL-1

; CURRENT APPLICATION NUMBER: US/10/293,992

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/434,193

; PRIOR FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/107,219

; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 3

; LENGTH: 516

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(516)

; OTHER INFORMATION:

US-10-293-992-3

Query Match

Best Local Similarity 73.8%; Score 516; DB 13; Length 516;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAACCTAAGGTCCTCTGAACCCCTCATGGAATAGATATTAAAGGAGAG 60
 Db 1 GTCCCTCAGAACCTAAGGTCCTCTGAACCCCTCATGGAATAGATATTAAAGGAGAG 60

Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120

Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 120
QY 121 CACAATGGAGCGCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
Db 121 CACAATGGAGCGCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
QY 181 GAGACAGTGGGAATACAAATGTCAGCACCACCAAGTTAAATGAGAGTGAACCTGTGTAC 240
Db 181 GAGACAGTGGGAATACAAATGTCAGCACCACCAAGTTAAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 300
Db 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 300
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGAGTGTGTGTGTGTGTGTGTGTGT 360
Db 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGAGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACAATCTCCATTAACAAT 420
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACAATCTCCATTAACAAT 420
QY 421 GCCACAGTTGAAGACAGTGAAGTCTTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGT 480
Db 421 GCCACAGTTGAAGACAGTGAAGTCTTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGT 480
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 13

US-09-944-277A-10
; Sequence 10, Application US/09944277A
; Patent No. US20020034771A1

GENERAL INFORMATION:

APPLICANT: Frank, Glenn P.
Porter, James P.
Rushlow, Keith E.
Wassom, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,277A
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873
FILING DATE: 1999-03-31
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 nucleotides
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..591
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 73.8%; Score 516; DB 9; Length 591;

Best Local Similarity 100.0%; Pred. No. 5.9e-158; Mismatches 0; Indels 0; Gaps 0;
Matches 516; Conservative 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
Db 76 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAAAGTTTGAATATTTGTAATGCCAAATTT 180
Db 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAAAGTTTGAATATTTGTAATGCCAAATTT 255
QY 181 GAGACAGTGGAGAAATACAAATGTGAGCACAACAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 256 GAGACAGTGGAGAAATACAAATGTGAGCACAACAAGTTAATGAGAGTGAACCTGTGTAC 315
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 300
Db 316 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 375
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGAGTGTGTGTGTGTGTGTGTGTGTAT 360
Db 376 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGAGTGTGTGTGTGTGTGTGTGTAT 435
QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACAATCTCCATTAACAAT 420
Db 436 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACAATCTCCATTAACAAT 495
QY 421 GCCACAGTTGAAGACAGTGAAGTCTTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 480
Db 496 GCCACAGTTGAAGACAGTGAAGTCTTCTTTCAGGCTCTCTCTGAGTGTGTGTGTGTGTGT 555
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516
Db 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591

RESULT 14

US-09-809-715-3
; Sequence 3, Application US/09809715
; Publication No. US20030003502A1

GENERAL INFORMATION:

APPLICANT: Jaretzky, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Wurzburg, Beth A.
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC
TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
TITLE OF INVENTION: ANTIBODY AND USES THEREOF

FILE REFERENCE: AL-8

CURRENT APPLICATION NUMBER: US/09/809,715

CURRENT FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/189,853

PRIOR FILING DATE: 2000-03-15

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 3

LENGTH: 528

TYPE: DNA

ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(528)
US-09-809-715-3

Query Match      73.7%; Score 515.2; DB 10; Length 528;
Best Local Similarity 98.5%; Pred. No. 1e-157;
Matches 520; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGTCCTCTGGAACCTCCATGGAATGAATATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAACCTAAGGTCCTCTGGAACCTCCATGGAATGAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 120

QY 121 CACATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180
Db 121 CACATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180

QY 181 GAAGACAGTGAGAGATACAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 GAAGACAGTGAGAGATACAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 241 CTGGAAGTCTTCAAGTACTGCTGCTCTTCCAGGCCTCTGCTGAGGTGGTGGAGGGC 300
Db 241 CTGGAAGTCTTCAAGTACTGCTGCTCTTCCAGGCCTCTGCTGAGGTGGTGGAGGGC 300

QY 301 CAGCCCTCTTCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 CAGCCCTCTTCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 361 TATAAGGATGTGAGAGTCTTCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TATAAGGATGTGAGAGTCTTCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

QY 421 GCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGT 480
Db 421 GCGCAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGT 480

QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGGCTGAGAGAG 528
Db 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGGCTGAGAGAG 528

RESULT 15
US-10-236-392-29
; Sequence 29, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Viadimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Pasturajan, Meera
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; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shency, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 29
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(680)
US-10-236-392-29

Query Match      65.1%; Score 455; DB 13; Length 757;
Best Local Similarity 83.3%; Pred. No. 7e-138;
Matches 582; Conservative 0; Mismatches 0; Indels 117; Gaps 1;

QY 1 GTCCCTCAGAACCTAAGGTCCTCTGGAACCTCCATGGAATGAATATTTAAAGGAGAG 60
Db 101 GTCCCTCAGAACCTAAGGTCCTCTGGAACCTCCATGGAATGAATATTTAAAGGAGAG 160

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 120
Db 161 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 220

QY 121 CACATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180
Db 221 CACATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 280

QY 181 GAAGACAGTGAGAGATACAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 281 GAAGACAGTGAGAGATACAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301

QY 241 CTGGAAGTCTTCAAGTACTGCTGCTCTTCCAGGCCTCTGCTGAGGTGGTGGAGGGC 300
Db 302 CTGGAAGTCTTCAAGTACTGCTGCTCTTCCAGGCCTCTGCTGAGGTGGTGGAGGGC 301

QY 301 CAGCCCTCTTCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 302 CAGCCCTCTTCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343

QY 361 TATAAGGATGTGAGAGTCTTCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
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Db	344	TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT	403
Qy	421	GCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGACTAT	480
Db	404	GCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGACTAT	463
Qy	481	GAGTCTGAGCCCTCAACATTACTGTATAAAAGCTCCGCGTGAGAGTACTGGCTACAA	540
Db	464	GAGTCTGAGCCCTCAACATTACTGTATAAAAGCTCCGCGTGAGAGTACTGGCTACAA	523
Qy	541	TTTTTATCCCATTTGTTGGTGGTATCTCTTGAAGATTAAAGATTAAGAACCCAGGAAGGCTTCAGACTT	600
Db	524	TTTTTATCCCATTTGTTGGTGGTATCTCTTGAAGATTAAAGATTAAGAACCCAGGAAGGCTTCAGACTT	583
Qy	601	ACTCAGCAGCAGTCACTTCTCTTGAAGATTAAAGATTAAGAACCCAGGAAGGCTTCAGACTT	660
Db	584	ACTCAGCAGCAGTCACTTCTCTTGAAGATTAAAGATTAAGAACCCAGGAAGGCTTCAGACTT	643
Qy	661	CTGAACCCACATCCTAAGCCAAACCCCAAAACAACTGA	699
Db	644	CTGAACCCACATCCTAAGCCAAACCCCAAAACAACTGA	682

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Job time : 408.226 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 2358.62 Seconds
(without alignments)
8849.962 Million cell updates/sec

Title: US-10-763-400-7
Perfect score: 699
Sequence: 1 gtccctcagaacctaaagt.....caaaccccaaaactga 699

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: em_estba.*

2: em_estum.*

3: em_estin.*

4: em_estov.*

5: em_estpl.*

6: em_estro.*

7: em_estro.*

8: em_estro.*

9: gb_estl.*

10: gb_estl.*

11: gb_estl.*

12: gb_estl.*

13: gb_estl.*

14: gb_estl.*

15: em_estfun.*

16: em_eston.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gssl.*

29: gb_gssl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	615.8	88.1	810	12	BG542554
2	559.4	80.0	760	12	BG542157
3	533	76.3	834	10	BF679057
4	480.6	68.8	840	12	BG548515

C	5	475.4	68.0	768	13	BQ573778
C	6	436.6	62.5	846	10	BF678252
C	7	417	59.7	707	14	CA448745
C	8	411.6	58.9	712	14	CA419024
C	9	367.6	52.6	669	10	AW612525
C	10	350.6	50.2	818	10	BF677190
C	11	326.4	46.7	615	12	BM991911
C	12	308.4	44.1	488	13	EX110472
C	13	296	42.3	660	14	CF362072
C	14	254	36.3	570	9	AI676114
C	15	250.8	35.9	652	13	BY752906
C	16	250	35.8	651	14	CF363368
C	17	244.2	34.9	540	9	AI685796
C	18	225.4	32.2	641	14	CB429248
C	19	212.6	30.4	394	10	AW357271
C	20	186	26.6	479	10	BF593204
C	21	184	26.3	478	12	BQ005218
C	22	180.4	25.8	757	14	CA508723
C	23	178.2	25.5	422	10	BF603113
C	24	175.8	25.2	403	14	CB768694
C	25	173	24.7	446	9	AI676097
C	26	169	24.2	848	14	CB958187
C	27	168.6	24.1	1033	9	AL549464
C	28	168.6	24.1	1201	9	AL531122
C	29	167	23.9	874	14	CD244068
C	30	167	23.9	1201	13	BX399366
C	31	166.2	23.8	1201	9	AL514096
C	32	163	23.3	823	12	BI768140
C	33	162.2	23.2	1201	13	EX402696
C	34	161.4	23.1	664	14	CB555672
C	35	161.4	23.1	987	13	EX435202
C	36	160.4	22.9	852	12	BI821954
C	37	156.6	22.4	528	14	CB152997
C	38	154.8	22.1	571	14	CD693938
C	39	154.6	22.1	640	9	AUI37840
C	40	154.4	22.1	1201	9	AL558081
C	41	151.4	21.7	344	12	BI341697
C	42	150.6	21.5	429	13	BY228345
C	43	148.8	21.3	551	12	BM364531
C	44	144.8	20.7	270	10	AW357272
C	45	143.6	20.5	812	13	EX378677

ALIGNMENTS

RESULT 1

BG542554

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG542554 810 bp mRNA linear EST 03-APR-2001
602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5',
mRNA sequence.
BG542554
BG542554.1 GI:13534787
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 810)

NIH-MGC <http://mgi.nci.nih.gov/>

National Institutes of Health

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Cloned through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: LLC1523 row: h column: 14

High quality sequence stop: 667.

FEATURES
source

Location/Qualifiers

1. .810
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4695476"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGCGCCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 88.1%; Score 615.8; DB 12; Length 810;
Best Local Similarity 96.7%; Pred. No. 2.1e-171;
Matches 672; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

QY 1 -GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCATGGAATAGATAATTTAAAGGAGAG 60
Db |
QY 106 GTCCTCAGAACCTTAAGTCTCTTGAACCCCTCATGGAATAGATAATTTAAAGGAGAG 165
Db |
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db |
QY 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 225
Db |
QY 121 CACATGCGAGCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGTCAGTCCAAATTT 180
Db |
QY 226 CACATGCGAGCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGTCAGTCCAAATTT 285
Db |
QY 181 GAAGACAGTGGAGATACAAATGTGACACCAACAAAGTTAATGAGATGAACCTGTGTAC 240
Db |
QY 286 GAAGACAGTGGAGATACAAATGTGACACCAACAAAGTTAATGAGATGAACCTGTGTAC 345
Db |
QY 241 CTGGAAGTCTTCAGTACAGTGGTCTCTTCTGAGGCTCTGCTGAGGTGGTATGGAGGC 300
Db |
QY 346 CTGGAAGTCTTCAGTACAGTGGTCTCTTCTGAGGCTCTGCTGAGGTGGTATGGAGGC 405
Db |
QY 301 CAGCCCTCTTCTCAGTGGCATGTTGGAGGAACCTGGATGTGTACAGGTGATCTAT 360
Db |
QY 406 CAGCCCTCTTCTCAGTGGCATGTTGGAGGAACCTGGATGTGTACAGGTGATCTAT 465
Db |
QY 361 TATAAGGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATPACAAAT 420
Db |
QY 466 TATAAGGATGTGAAGTCTCAAGTACTGTGTATGAGAACCAACATCTCCATPACAAAT 525
Db |
QY 421 GCCCAGTGTGAAGACAGTGGTACTTCTGTCAGGCGCAAGTGTGCGAGCTGGACTAT 480
Db |
QY 526 GCCCAGTGTGAAGACAGTGGTACTTCTGTCAGGCGCAAGTGTGCGAGCTGGACTAT 585
Db |
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGGTGTGAGAGTACTGGCTACAA 540
Db |
QY 586 GAGTCTGAGCCCTCAACATTTACTGT-ATAAAGCTCCGGTGTGAGAGTACTGGCTACCA 644
Db |
QY 541 TTTTATATCCATTTGGTGGTGAATCTGTTTCTGCTGTGGACAC--AGGATTTATCT 598
Db |
QY 645 ATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGCTGTGGACACACAGGGATTTATCT 704
Db |
QY 599 -CAACTCAGCAGCAGGTACATTTCTC--TTGAAGATTAAGAGAACCAAGAAAGGCTTCA 655
Db |
QY 705 CCAACTCAGCAGCAGGTACATTTCTCTCTTGACGATTAGAGAACCCGGAAGGGCTCA 764
Db |
QY 656 GACTTCTGAACCCACATCTTAAGCCAAACCCAAA 690
Db |
QY 765 GACTCCTGAACCCCAATTCCTAAGACAAACCCAAA 799
Db |

RESULT 2
LOCUS

DEFINITION BG542157 760 bp mRNA linear EST 03-APR-2001
602571381F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695476 5',
mRNA sequence.

ACCESSION

VERSION BG542157 GI:13534390

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov

REFERENCE

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1521 row: b column: 21

High quality sequence stop: 751.

FEATURES

source

1. .760
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4695476"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGCGCCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 80.0%; Score 559.4; DB 12; Length 760;

Best Local Similarity 98.5%; Pred. No. 1.2e-154;

Matches 596; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY 92 TCTTTGAAGTCCAGTCCACCAATGCTTCCAAATGGCAGCGCTTTCAGAGAGACAAAT 151
Db |
QY 98 TGTTAGAGTCAAGTCCACCAATGCTTCCAAATGGCAGCGCTTTCAGAGAGACAAAT 157
Db |
QY 152 CAAAGTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 211
Db |
QY 158 CAAAGTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 217
Db |
QY 212 AACAGTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 271
Db |
QY 218 AACAGTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGACC 277
Db |
QY 272 AGGCTCTGCTGAGTGGTGTGATGGAGCGCCAGCCCTCTTCTCAGTGGCATGCTTGA 331
Db |
QY 278 AGGCTCTGCTGAGTGGTGTGATGGAGCGCCAGCCCTCTTCTCAGTGGCATGCTTGA 337
Db |
QY 332 GGAATCTGGATGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGT 391
Db |
QY 338 GGAATCTGGATGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGT 397
Db |
QY 392 ATGAGAACCAACATCTCCATTTACAAATGCCAGTGTGAAGACAGTGGAACTACTACT 451
Db |

Db 398 ATGAGAACCAACATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTACTACT 457
Qy 452 GTACGGGCAAGTGTGGCAGCTGATGAGTCTGAGCCCTCAACATCTGTAATAA 511
Db 458 GTACGGGCAAGTGTGGCAGCTGATGAGTCTGAGCCCTCAACATCTGTAATAA 517
Qy 512 AAGCTCCGCTGAGAGTACTGGCTACAAATTTTATCCCAATGTTGGTGGTGAATCTGT 571
Db 518 AAGCTCCGCTGAGAGTACTGGCTACAAATTTTATCCCAATGTTGGTGGTGAATCTGT 576
Qy 572 TTGCTGTGGACACAGGATTTATCTCACTCAGCAGAGGTCACATTTCTCTTGAAGA 631
Db 577 TTGCTGTGGACACAGGATTTATCTCACTCAGCAGAGGTCACATTTCTCTTGAAGA 636
Qy 632 TTAAGAGAACCAAGAAAG-GCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAA 690
Db 637 TTAAGAGAACCAAGAAAGGCTTCAGACTTCTGAACCCCA-ATCCTAAGCCAAACCCGAA 695
Qy 691 AACAA 695
Db 696 AAAA 700

RESULT 3
BF679057
LOCUS 602153315F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294467 5',
DEFINITION mRNA sequence.
ACCESSION BF679057
VERSION BF679057.1 GI:11952952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1143 row: n column: 04
High quality sequence stop: 621.
Location/Qualifiers
1. 834
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294467"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

FEATURES

source
1. 834
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294467"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Query Match 76.3%; Score 533; DB 10; Length 834;
Best Local Similarity 95.3%; Pred. No. 8.8e-147;

Matches 582; Conservative 0; Mismatches 25; Indels 4; Gaps 3;
Qy 1 GTCCCTCAGAAACCTTAAGGTCTCCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 60
Db 106 GTCCCTCAGAAACCTTAAGGTCTCCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 165
Qy 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
Db 166 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 225
Qy 121 CACAATGCGAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 180
Db 226 CACAATGCGAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 285
Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAATGAGAGTGAACCTGTGTAC 240
Db 286 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAATGAGAGTGAACCTGTGTAC 345
Qy 241 CTGGAAGTCTTTCAGTGAAGTGGCTCTCCTTCAGGCTCTGCTGAGTGGTGGTGGAGGCG 300
Db 346 CTGGAAGTCTTTCAGTGAAGTGGCTCTCCTTCAGGCTCTGCTGAGTGGTGGTGGAGGCG 405
Qy 301 CAGCCCTCTTCTCCTCAGGTGGCCATGTTGGAGGAACTGGGATGTGTACAAGTGTATCTAT 360
Db 406 CAGCCCTCTTCTCCTCAGGTGGCCATGTTGGAGGAACTGGGATGTGTACAAGTGTATCTAT 465
Qy 361 TATAAGGATGTTGAAGTCTCTCAAGTACTGTTATGAGAACCAACATCTCCATTACAAAT 420
Db 466 TATAAGGATGTTGAAGTCTCTCAAGTACTGTTATGAGAACCAACAA-ATCTCCATTACAAAT 524
Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTTCTAGCGGCAAGTGTGGCAGCTGGACTAT 480
Db 525 GCCACAGTTGAAGACAGTGGAACTTACTTCTAGCGGCAAGTGTGGCAGCTGGACTAT 584
Qy 481 GAGTCTGAGCCCTCAACATTTACTATAAAAGTCCCGTGAAGAGTACTGGGTACAA 540
Db 585 GAGTCTGAG-CCCTCAACATTTACTGTATAAAAGTCCCGTGAAGAGTACTGGGTACAA 643
Qy 541 TTTTATATCCCAT--GTTGGTGGTGGTCTCTTTGCTGTGGACACAGATTTATCT 598
Db 644 ATTATATCCCAATGGTGGCGTGAATTTCTGTTGGCGTGGACACAGCTTATATCT 703
Qy 599 CAACCTCAGCAG 609
Db 704 TCATCAGCGG 714

RESULT 4

BF679057

LOCUS 602153315F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4704624 5',

DEFINITION mRNA sequence.

ACCESSION BF679057

VERSION BF679057.1 GI:13547180

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 840)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM1544 row: p column: 01

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High quality sequence stop: 590.
FEATURES
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      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4704624"
      /lab_host="DH10B (TI phage-resistant)"
      /clone_lib="NIH_MGC_77"
      /note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site 1:
      3' adaptor used in cloning as follows: 5' adaptor
      sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
      5'-ATCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,
      C, or G and N = A, C, G, or T). Average insert size 1.9
      kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
      by PCR. This library was enriched for full-length clones
      and was constructed by Clontech Laboratories (Palo Alto,
      CA). Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      68.8%; Score 480.6; DB 12; Length 840;
  Best Local Similarity 87.1%; Pred. No. 3.3e-131;
  Matches 626; Conservative 0; Mismatches 69; Indels 24; Gaps 8;

QY 1 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
   |||||
Db 106 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 165
   |||||
QY 51 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
   |||||
Db 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGTTTC 225
   |||||
QY 121 CACAATGCGAGCTTTTCAAGAGAGACAATTCAGATTTGAATATTGTAATGCCAATTT 180
   |||||
Db 226 CACAATGCGAGCTTTTCAAGAGAGACAATTCAGATTTGAATATTGTAATGCCAATTT 285
   |||||
QY 181 GAAGACAGTGAGAGATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240
   |||||
Db 286 GAAGACAGTGAGAGATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 345
   |||||
QY 241 CTGGAAGTCTTCAGTGAAGTCTCTCTCTCAGGCTCTGTCAGTGGTGGTGAAGGAGGC 300
   |||||
Db 346 CTGGAAGTCTTCAGTGAAGTCTCTCTCTCAGGCTCTGTCAGTGGTGGTGAAGGAGGC 405
   |||||
QY 301 CAGCCCTCTCTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360
   |||||
Db 406 CAGCCCTCTCTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 465
   |||||
QY 361 TATAGAGTGTGAGAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCT 420
   |||||
Db 466 TATAGAGTGTGAGAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCT 525
   |||||
QY 421 -GCCACAGTTTGAAGACAGTGGAACTTAC-TACTGTACGGGCAAGTGGTGGTGGTGGTGG 477
   |||||
Db 526 TGCCACAGTTTGAAGACAGTGGAACTTAC-TACTGTACGGGCAAGTGGTGGTGGTGGTGG 585
   |||||
QY 478 -----TATAGTCTGAGCCCTCAACATTTACTGTAA-----TAAAGCTCCGGT-- 522
   |||||
Db 586 CTATGAGTCTGAGCCCTCAACATTTACTGTAA-----TAAAGTCTCCGGTGA 645
   |||||
QY 523 -GAGAAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAAT--CGTTTGGTGG 579
   |||||
Db 646 AGAAGTACTTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCCCTTGGTGGTGG 705
   |||||
QY 580 GACACAGGA-TTATTTATCTCAACTCAGCA--GCAGGTCACTTTCTCTTTGAAGATTAG 636
   |||||
Db 706 CACCCCGAATTATTTATCTCAACTCAGCA--GCAGGTCACTTTCTCTTTGAAGATTAG 765
   |||||
QY 637 AGRACAGGAAGCTTCAGACTTCTGAACCCACATCTTAAGCCAAACCCCAACAA 695
   |||||
Db 766 GAAACCCAGGAAGCTTCAGAAATTTTGAACCCAAATCTTAGGCAAAACCCCAACAA 824
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RESULT 5
BQ573778/c
LOCUS
DEFINITION
UI-H-EZO-bav-1-04-0-UI.s1 NCI CGAP Chl Homo sapiens cDNA clone
UI-H-EZO-bav-1-04-0-UI 3', mRNA sequence.
ACCESSION
BQ573778.1 GI:21477095
VERSION
BQ573778.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 768)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-41, >AT-rich#Low complexity (matched complement)
93-129, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..768
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZO-bav-1-04-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Chl"
/note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Chl is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCCT.
TAG_ISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZO
TAG_SEQ=ATCTAATATG

Query Match 68.0%; Score 475.4; DB 13; Length 768;
Best Local Similarity 99.6%; Pred. No. 1.1e-123;
Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
QY 222 TGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTGAAGTGGTGGTGGTGGTGGTGGTGG 281
|||
Db 768 TGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTGAAGTGGTGGTGGTGGTGGTGGTGG 709
|||
QY 282 TGAGTGTGTGTAGGAGCGGCGAGCCCTCTTCTCAGTGGCATGTTGGAGGACTGGGA 341
|||
Db 708 TGAGTGTGTGTAGGAGGCGGCGAGCCCTCTTCTCAGTGGCATGTTGGAGGACTGGGA 649
|||

QY 342 TGTGTCAAGGTGATCTATTATAGGATGTTGAAGCTCTCAAGTACTGGTATGAGAACA 401
 Db 648 TGTGTCAAGGTGATCTATTATAGGATGTTGAAGCTCTCAAGTACTGGTATGAGAACA 589
 QY 402 CAACATCTCCATTAACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAA 461
 Db 588 CAACATCTCCATTAACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAA 529
 QY 462 AGTGTGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTATTAATTAAGCTCCGG 521
 Db 528 AGTGTGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTATTAATTAAGCTCCGG 469
 QY 522 TGAGAAGTACTGGTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGTGGA 581
 Db 468 TGAGAAGTACTGGTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGTGGA 409
 QY 582 CACAGGATTAATTAATCACTCAGCAGAGGTGACATTTCTTGAAGATTAAGAGAAC 641
 Db 408 CACAGGATTAATTAATCACTCAGCAGAGGTGACATTTCTTGAAGATTAAGAGAAC 349
 QY 642 CAGGAAGGCTTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699
 Db 348 CAGGAAGGCTTCAGACTCTTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 291

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 LOCUS 60208616F1 NIH_MGC_83 846 bp mRNA linear EST 21-DEC-2000
 DEFINITION 60208616F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5',
 mRNA sequence.
 ACCESSION BF678252
 VERSION BF678252.1 GI:11952147
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 846)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM1071 row: j column: 15
 High quality sequence stop: 609.
 Location/Qualifiers
 1..846
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4250222"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfII (ggcgctcgcc); Site 2: SfiI
 (ggcattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CAGCGCATTAAGGCC-3'
 and 3' adaptor sequence:
 5'-ATTATGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA).

FEATURES

source
 1..846
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4250222"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfII (ggcgctcgcc); Site 2: SfiI
 (ggcattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CAGCGCATTAAGGCC-3'
 and 3' adaptor sequence:
 5'-ATTATGAGCGGCGGCGGCATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA).

ORIGIN

Query Match 62.5%; Score 436.6; DB 10; Length 846;
 Best Local Similarity 92.1%; Pred. No. 4e-118;
 Matches 572; Conservative 0; Mismatches 34; Indels 15; Gaps 10;
 QY 1 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCTCATGGAATAGATATTAA-AGGAGA 59
 Db 100 GTCCCTCAGAAACCTAAGTCTCTTGAACCTCTCATGGAATAGATATTAA-AGGAGA 159
 QY 60 GAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAAGTCCACCAATGGTT 119
 Db 160 GAATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAAGTCCACCAATGGTT 219
 QY 120 CCACAAATGCCAGCCCTTCAGAAAGACAAATTCAGTTTGAATTTGAATTTGGAATGCAAAATT 179
 Db 220 CCACAAATGCCAGCCCTTCAGAAAGACAAATTCAGTTTGAATTTGAATTTGGAATGCAAAATT 277
 QY 180 TGAGACACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTA 239
 Db 278 TGAGACACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTA 337
 QY 240 CTTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTCTGAGGTTGATGGAGGG 299
 Db 338 CTTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGCCCTCTCTGAGGTTGATGGAGGG 396
 QY 300 CCAGCCCTCTTCTCAGTGGCCATGGTTGAGGAACCTGGGATGTGTACAAAGGTGATCTA 359
 Db 397 CCAGCCCTCTTCTCAGTGGCCATGGTTGAGGAACCTGGGATGTGTACAAAGGTGATCTA 455
 QY 360 TTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAACATCTCCATTACAAA 419
 Db 456 TTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAACATCTCCATTACAAA 513
 QY 420 TGCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGAGCTGGACTA 479
 Db 514 TGCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGAGCTGGACTA 571
 QY 480 TGAGTCTCAGCCCTCAACATTTACTGTATATAAGCTCCGGTGAAGAGTACTGGCTACA 539
 Db 572 TGAGTCTCAGCCCTCAACATTTACTGTATATAAGCTCCGGTGAAGAGTACTGGCTACA 631
 QY 540 ATTTTATATCCCATTTGTTGGTGGATTTCTGTTTCTGTGGACACAGAGTATTATTTATCTC 599
 Db 632 CTTTATATCCCATTTGTTGGGATTTCTGTTTCTGTGGACACAGAGTATTATTTATCTC 685
 QY 600 AACTCAGCAGCAGGTGCACATT 620
 Db 686 AACTCAGCAGCAGGTGCACATT 706
 RESULT 7
 CA448745/c
 LOCUS CA448745.1
 DEFINITION UI-H-E10-ayo-p-24-0-UI.s1 NCI CGAP_E10 Homo sapiens cDNA clone
 UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.
 ACCESSION CA448745
 VERSION CA448745.1 GI:24813165
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 707)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 93-129, >LINE2 (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..707
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E10-avo-p-24-0-UI"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP E10"
 /note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP E10 is a cDNA library containing the following
 tissue(s): Chondrosarcoma. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into p7T3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is ACATTGCAC.
 TAG_TISSUE=chondrosarcoma
 TAG_LIB=UI-H-E10
 TAG_SEQ=ACATTGCAC"

ORIGIN

Query Match 59.7%; Score 417; DB 14; Length 707;
 Best Local Similarity 100.0%; Pred. No. 2.4e-112; Mismatches 0; Indels 0; Gaps 0;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 283 GAGTGGTGTGAGGGGCGAGCCCTCTCTCTCAGGTGCCATGTTGGAGAACTGGGAT 342
 DB 707 GAGTGGTGTGAGGGGCGAGCCCTCTCTCTCAGGTGCCATGTTGGAGAACTGGGAT 648
 QY 343 GTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTCTGATGAGAACAC 402
 DB 647 GTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTCTGATGAGAACAC 588
 QY 403 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAA 462
 DB 587 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAA 528
 QY 463 GTGTGGCAGTGGAGTATGAGTCTGAGCCCTCAACATTAATGTAATAAAGTCCCGGT 522
 DB 527 GTGTGGCAGTGGAGTATGAGTCTGAGCCCTCAACATTAATGTAATAAAGTCCCGGT 468
 QY 523 GAGAGTACTGCTACATATTTTATCCATGTTGTTGGTGGTCTGTTGCTGGAC 582
 DB 467 GAGAGTACTGCTACATATTTTATCCATGTTGTTGGTGGTCTGTTGCTGGAC 408
 QY 583 ACAGATTATTATCTCAACTCAGCAGAGGTCACTTTCTCTTGAAGATTAAAGAGAAC 642
 DB 407 ACAGATTATTATCTCAACTCAGCAGAGGTCACTTTCTCTTGAAGATTAAAGAGAAC 348
 QY 643 AGGAAGGCTTCAGACTCTGAAGCCCATCTTAAGCCCAACCCCAAAACACTGA 699
 DB 347 AGGAAGGCTTCAGACTCTGAAGCCCATCTTAAGCCCAACCCCAAAACACTGA 291

RESULT 8

CA419024/c

LOCUS

DEFINITION

ACCESSION

VERSION

CA419024 712 bp mRNA linear EST 07-NOV-2002
 UI-H-E21-bbj-e-19-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone
 UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.
 CA419024
 CA419024.1 GI:24781675

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of

Orthopaedics

cDNA library preparation: Dr. M. Bento Soares, University of Iowa

cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA

sequence: 1-42, >(TAAA)n#Simple_repeat (matched complement)

94-130, >LINE2 (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..712

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-E21-bbj-e-19-0-UI"

/tissue_type="Chondrosarcoma Grade II"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP Ch2"

/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI CGAP Ch2 is a normalized cDNA library containing the

following tissue(s): Chondrosarcoma Grade II. The library

was constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into p7T3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is

TCATCAGCT.

TAG_TISSUE=grade-2-chondrosarcoma

TAG_LIB=UI-H-E21

TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 58.9%; Score 411.6; DB 14; Length 712;
 Best Local Similarity 98.3%; Pred. No. 9.7e-111;
 Matches 414; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 279 TGCTGAGTGGTGTGAGGGCGAGCCCTCTCTCTCAGGTGCCATGTTGGAGAACTG 338
 DB 712 TGCTGAGTGGTGTGAGGGCGAGCCCTCTCTCTCAGGTGCCATGTTGGAGAACTG 653
 QY 339 GGATGTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTGTTAGAA 398
 DB 652 GGATGTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTGTTAGAA 593
 QY 399 CCACAACTCTCCATTACAAATGCCACAGTGAAGACAGTGAACCTACTACTGTACGGG 458
 DB 592 CCACAACTCTCCATTACAAATGCCACAGTGAAGACAGTGAACCTACTACTGTACGGG 533
 QY 459 CAAAGTGGCGAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTAAATAAGCTCC 518
 DB 532 CAAAGTGGCGAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTAAATAAGCTCC 473


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QY 519 GCGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGT 578
Db 472 GCGTGAGAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGGTGAATCTGTTTCTGT 413
QY 579 GGACACAGGATTTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAAGAG 638
Db 412 GGACACAGGATTTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAAGAG 353
QY 639 AACACAGAAAGGTTTCAGATCTTGTGAACCCACATCTTAAGCCAAACCCCAAAACAACTG 698
Db 352 AACACAGAAAGGTTTCAGATCTTGTGAACCCACATCTTAAGCCAAACCCCAAAACAACTG 293
QY 699 A 699
Db 292 A 292

RESULT 9
AW612525/c 669 bp mRNA linear EST 23-MAR-2000
LOCUS h03f07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2954053 3'
DEFINITION similar to gp:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
ALPHA-SUBUNIT (HUMAN); mRNA sequence.
ACCESSION AW612525
VERSION AW612525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 669)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 438.
FEATURES
source
1..669
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2954053"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Kid11"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following RAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 132376-132391, 145600-145675, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
ORIGIN
Query Match 52.6%; Score 367.6; DB 10; Length 669;
Best Local Similarity 97.2%; Pred. No. 1.1e-97;
Matches 384; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
QY 306 CCTCTTCTCAGGTCGCCATGTTTATCCCATTTGTTGGTGGTGAATCTTATTATAA 365

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Db 669 CCTCTTCTCAGGTCGCCATGTTTATCCCATTTGTTGGTGGTGAATCTTATTATAA 610
QY 366 GGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACACACATCTCCATTAGAAATGCCAC 425
Db 609 GGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACACACATCTCCATTAGAAATGCCAC 550
QY 426 AGTTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTATGAGTC 485
Db 549 AGTTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTATGAGTC 490
QY 486 TGAGCCCTTCAACATTACTGTAAATAAAGTCCCGGTGAGAGTACTGGCTACAA-TTTT 544
Db 489 TGAGCCCTTCAACATTACTGTAAATAAAGTCTCTGGTGAAGTACTGGCTACAAATTTT 430
QY 545 TTATCCCATTTGTTGGTGGTGTCTGTGTCGACACAGGATTATTATCTCAACTC 604
Db 429 TTATCCCATTTGTTGGTGGTGTCTGTGTCGACACAGGATTATTATCTCAACTC 370
QY 605 AGCAGCAGTCTCACTTTCTTTGAAGATTAAGAGAACCCAGGAAGGCTTCAGACTCTGA 664
Db 369 AGCAGCAGTCTCACTTTCTTTGAAGATTAAGAGAACCCAGGAAGGCTTCAGACTCTGA 310
QY 665 ACCACATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 309 ACCACATCTTAAGCCAAACCCCAAAACAACTGA 275

RESULT 10
BF677190 818 bp mRNA linear EST 21-DEC-2000
LOCUS 60208725F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251469 5',
DEFINITION mRNA sequence.
ACCESSION BF677190
VERSION BF677190
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 818)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1074 row: n column: 14
High quality sequence stop: 616.
FEATURES
source
1..818
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4251469"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: Prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccattatggcc); Site 2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCCATATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCCGACATG-(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

```

ORIGIN

Query Match 50.2%; Score 350.6; DB 10; Length 818;
 Best Local Similarity 83.2%; Pred. No. 1.4e-92;
 Matches 520; Conservative 0; Mismatches 89; Indels 16; Gaps 10;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 60
 Db 110 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 169

QY 61 AATGTGACTTTACATGTAATGGGACAAATTCCTT-TGAAGTCAGTTCACCAATGGTT 119
 Db 170 AATGTGACTTTACATGTAATGGGACAAATTCCTT-TGAAGTCAGTTCACCAATGGTT 229

QY 120 CCACAAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATA----TTGTGAATGCCA 175
 Db 230 CCACAAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATGCCA 289

QY 176 AAT--TTGAAGACAGTGGAGAAAT-ACAAATGTCAGACACAAATGTAATGAGAGTGAAC 232
 Db 290 AATGTGAAACAGTGGGCAATACAAATGTCAGACACAAATGTAATGAGAGTGAAC 349

QY 233 CTGTGACTGGAAGTCTTCACTGAGTGGCTCTTCAAGGCTCTCTGAGTGGTGA 292
 Db 350 CTGTGACTGGAAGTCTTCACTGAGTGGCTCTTCAAGGCTCTCTGAGTGGTGA 409

QY 293 TGGAGGGCCAGCCCTCTTCTCAGTCCATGCTGAGTGGAGAACTGGGATGTGAC-AAAG 351
 Db 410 TGGAGGGCCAGCCCTCTTCTCAGTCCATGCTGAGTGGAGAACTGGGATGTGAC-AAAG 469

QY 352 GTGATCTATTATTAAGGATGGTCAAGTCTCAAGTCTGATGAGACCAACATCTCC 411
 Db 470 GTGATCTATTATTAAGGATGGTCAAGTCTCAAGTCTGATGAGACCA-AAAATTTCC 527

QY 412 ATTCAAAATGCCACAGTGGAGACAGTGGAAACC---TACTACTGTACGGGCAAA-GTGTG 467
 Db 528 ATTCAAAATGCCACAGTGGAGACAGTGGAAACCCTAATCTTGTACGGGCAAAAGTGTG 587

QY 468 GCAGTGGACTTA-TGAGTCTGAGCCCTCAACATTAATGTAATGAAAGCTCCGGTGGAGA 526
 Db 588 GCAAGTGGACTTAATGAGTCTTGAAGCTTCAACATTAATGTAATGAAAGCTCCGGTGGAGA 647

QY 527 AGTACTGGCTACAATTTTATCCATGTTGGTGGTGAATCTCTGTTCTGTGACACAG 586
 Db 648 GAAAGTTACGGTACATTAATTAACCATGTTGGTGGTGAATCTGTTGGTGGAAAGG 707

QY 587 GATTATTATCTCAACTCAGCAGCA 611
 Db 708 GATTATTATTTCAATCGAAGGGCA 732

RESULT 11
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 LOCUS UI-H-DF1-auk-1-12-0-UI.s1 NCI CGAP_DFI Homo sapiens cDNA clone
 DEFINITION IMAGE:5870747 3', mRNA sequence.

ACCESSION BM991911
 VERSION BM991911.1 GI:19711300
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 615)
 NCBI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tissue Procurement: Dr. Jose Mercuende
 Tissue Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

REFERENCE
 AUTHORS NCI-CCAP
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 Tissue Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 The following repetitive elements were found in this cDNA
 sequence: 90-126, >LINE2 (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

Location/Qualifiers

1..615

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5870747"

/tissue_type="Subchondral Bone"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP DFI"

/note="Organ: Bone; Vector: p773-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 NCI CGAP DFI is a normalized cDNA library containing the
 following tissue(s): Subchondral Bone. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into p773-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (GT)₁₈ tail. The sequence tag for this library is
 GTTAAGCGTC.
 TAG_TISSUE=Subchondral bone
 TAG_LIB=UI-H-DF1
 TAG_SEQ=GTTAAGCGTC"

ORIGIN

Query Match 46.7%; Score 326.4; DB 12; Length 615;
 Best Local Similarity 99.7%; Pred. No. 1.9e-85;
 Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 372 TGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAATGCCACAGTTGA 431
 Db 615 TGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAATGCCACAGTTGA 556

QY 432 AGACAGTGAACCTACTACTGTACGGCAAGTGGCAGCTGGACTATGATCTGAGCC 491
 Db 555 AGACAGTGAACCTACTACTGTACGGCAAGTGGCAGCTGGACTATGATCTGAGCC 496

QY 492 CCTCAACATTACTGTAATAAAGCTCCGCGTGAAGAGTACTGGCTACAAATTTTATCCC 551
 Db 495 CCTCAACATTACTGTAATAAAGCTCCGCGTGAAGAGTACTGGCTACAAATTTTATCCC 436

QY 552 ATTGTGTGGTGAATCTGTTTGTGTGACACAGGATTTATCTCACTCAGCAGCA 611
 Db 435 ATTGTGTGGTGAATCTGTTTGTGTGACACAGGATTTATCTCACTCAGCAGCA 376

QY 612 GGTCACATTTCTCTTGAAGATTAAAGAACCAAGGAGGCTTCAGACTTCTGAAACCCACA 671
 Db 375 GGTCACATTTCTCTTGAAGATTAAAGAACCAAGGAGGCTTCAGACTTCTGAAACCCACA 316

QY 672 TCCTAAGCAAAACCCCAAAACAACTGA 699
 Db 315 TCCTAAGCAAAACCCCAAAACAACTGA 288

RESULT 12
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 DEFINITION IMAGE:2314294, mRNA sequence.
 ACCESSION BX110472
 VERSION BX110472.1 GI:27836404
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 488)
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radelof, U., Schneider, D. and Korn, B.
 TITLE Human Unigeneset - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGP98B235736.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/clonecards/cgi-bin/showlib.pl.cgi/?response?libNo=972 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCACAGGAACACGATTATGAC.
 FEATURES Location/Qualifiers
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 /sex="male"
 /dev_stage="adult"
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 /clone_lib="NCI CGAP Pr28"
 /notes="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; Plasmid DNA from the
 normalized library NCI CGAP Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneIDs
 983608-986759, 1101192-1101959, and 1217928-1220615).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 ORIGIN
 Query Match 44.1%; Score 308.4; DB 13; Length 488;
 Best Local Similarity 99.7%; Pred. No. 3,7e-80;
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 1 GTATGAGAACCAACATCTCCATTACAAATGCGACAGTGAACAGTGGACCTACTA 60
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 Qy 510 AAAAGCTCCGGTGGAGAGTACTGGCTACAAATTTTTATCCATTTGTTGGTGTGATCT 569
 Db 121 AAAAGCTCCGGTGGAGAGTACTGGCTACAAATTTTTATCCATTTGTTGGTGTGATCT 180
 Qy 570 GTTTGCTGTGACACAGGATTTATTTCTCACTCAGCAGAGTCACTTTCTTTGAA 629
 Db 181 GTTTGCTGTGACACAGGATTTATTTCTCACTCAGCAGAGTCACTTTCTTTGAA 240
 Qy 630 GATTAAAGAGAACCAAGAGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCAA 689
 Db 241 GATTAAAGAGAACCAAGAGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCAA 300
 Qy 690 AAACAACCTGA 699
 Db 301 AAACAACCTGA 310

RESULT 13
 CF362072
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CF362072 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA linear EST 25-AUG-2003
 CF362072 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.
 CF362072 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.
 CF362072.1 GI:34161364

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,
 Wiss, T.A., Nonnen, D.J., Wray, J.E. and Keale, J.W.
 A second set of porcine ESTs from a pooled-tissue normalized
 library
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: SRG8018 row: L column: 4
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 Location/Qualifiers
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 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including brain, liver, muscle, placenta/endometrium,
 ovary, testes, and bone marrow."

FEATURES
 source

Query Match 42.3%; Score 296; DB 14; Length 660;
 Best Local Similarity 71.6%; Pred. No. 2.1e-76;
 Matches 408; Conservative 0; Mismatches 150; Indels 12; Gaps 1;
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 Db 91 GTATCCAGGAATCTCAGGTGCTTGTATCCCCCATGGAATCGAATATTAGAGGAGAG 150
 Qy 61 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATTTGTTTC 120
 Db 151 AATGTGACTCTCAGATGTATTGGGAACGATGCTTGAATAATACCCCAATTTGGACA 210
 Qy 121 CACATGGCAGCTTTCAGAGAGACAATTCAGTTGAATTTGTGAATGCCAAATTT 180
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 Qy 241 CTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAGTGGTGTGAGGAGGC 300
 Db 331 CTGAAGTCACTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAGTGGTGTGAGGAGGC 390
 Qy 301 CAGCCCTCTTCTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTGTACAGGTGATCTAT 360
 Db 391 CAGTCTCTCTCCTCAGT 450
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACACATCTCCATTACAAAT 420

Db 451 TACAGGATGGAAAGCCCTCAGTACTGGTATGAGAACCAACCTCTCCATTACCAAT 510
 QY 421 GCACAGTTGAAGACAGTGGAACCTACTACTGTGTACGGCAAGTGTGCGACTGACTAT 480
 Db 511 GCCAAAAGAGAAGACAGTGGCTCTTATTGGTGCACGGGCATAAATTCAAAAATACCAAAA 570
 QY 481 GAGTCTGAGCCCTCAGCATTTACTCTAATAAAGCTCCGCT-----GAGAG 528
 Db 571 AACTCTACTACTCTCACCATTACCAACAAACAGATTCCCTTCAGTTCCTCGAACTAT 630
 QY 529 TACTGGCTACAAATTTTATCCCATTTGTTG 558
 Db 631 TACTGGCTACAGCTTCATATCCCATTTGTTG 660

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 LOCUS
 DEFINITION
 wc05e12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2314318 3',
 similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
 ALPHA-SUBUNIT (HUMAN);, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

A1676114 570 bp mRNA linear EST 17-DEC-1999
 A1676114.1 GI:4876594
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 EST.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE

1 (bases 1 to 570)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

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Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

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/clone_lib="NCI CGAP Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and ss

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (clones IDs

985608-986759, 1101192-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo.

ORIGIN

Query Match

Best Local Similarity 36.3%; Score 254; DB 9; Length 570;

Matches 275; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 390 GTATGAGAACCAACATCTCCATTACAATGCCAGTTGAGACAGTGGAACTACTA 449
 Db 570 GTAAGAAATCGCATCTGTGCCATAGCGAATGCCAGGTGATAGACAGTAGGCGCTATTG 511
 QY 450 CTGTACGGGCAAGAGTGTGCGAGCTGAGCTATGAGTCTGAGCCCCCTCAACATTACTGTAAT 509
 Db 510 CTGTGCGGCAAGAGTGTGCGAGCTGAGCTATGAGTCTGAGCCCCCTCAACATTACTGTAAT 451
 QY 510 AAAAGCTCGCGTGAAGTACTGGCTACAATTTTATCCCATTTGTTGGTGGTACTTCT 569
 Db 450 AAAAGCTCGCGTGAAGTACTGGCTACAATTTTATCCCATTTGTTGGTGGTACTTCT 391
 QY 570 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTACACATTTCCTTGAA 629
 Db 390 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTACACATTTCCTTGAA 331
 QY 630 GATTAAGAAACAGGAAAGGTTTCTGAGCTTCTGAAACCCACATCTTAGCCAAACCCCAA 689
 Db 330 GATTAAGAAACAGGAGAGGTTTCTGAGCTTCTGAAACCCACATCTTAGCCAAACCCCAA 271
 QY 690 AAACAACTCGA 699
 Db 270 AAACAGCTGA 261

RESULT 15

BY752906

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY752906 652 bp mRNA linear EST 17-DEC-2002
 BY752906 RIKEN full-length enriched, adult inner ear Mus musculus
 cDNA clone F930034C11 5', mRNA sequence.

BY752906

BY752906.1 GI:27184082

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 652)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Flotcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Korn, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

JOURNAL

MEDLINE

PUBMED

COMMENT

Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL: http://genome.gsc.riken.go.jp/
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Ito, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National
Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="F930034C11"
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ORIGIN

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Best Local Similarity 70.3%; Pred. No. 5.8e-63;
Matches 365; Conservative 0; Mismatches 148; Indels 6; Gaps 2;
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2 GCCACTGAGAAATCTGTACTGACCTTGGACCCCATGGATTAGAAATTTACAGAGAG 161
61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGT--CAGTCCACCAATGG 117
162 AAAGTGACCCCTTCTCTGTATGGGAAACAAATCACCTTCAATGAACCTCTACTACTAATGG 221
118 TTCCCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATTTGGAATGCCAAA 177
222 ATCCACATGGTACCGTCTCTGAGGTGAACCTTTCACATTTGGTCAITGTGAGTGCCACC 281
178 TTGGAAGCAGTGGAGATACAAATGTCAGGACCAACAAATTAATGAGATGAACCTGTG 237
282 GTTCAAGACAGTGGAAATATACATATGTCAGAGCAAGGATTTGTTTAAGAGTAAACCTGTG 341
238 TACCTGGAGTCTTTCAGTGACTGCTGCTCTTCAAGGCTCTGCTGAGTGGTGTGATGGAG 297
342 TACTTGAAATGTAACCAAGATTTGGTCTCTCTTCAGACATCTGTCACATGATCTTAGTC 401
298 G3CCAGCCCTCTTCTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAGGTGATC 357

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Db 462 TACTACAGAAATGACCATGCTTTTCACTACAGTTATGAGAGCC---CCGTCTCCATTAGA 518
Qy 418 AATGCCACAGTTTGAAGACAGTGGAAACCTTACTGTGTACGGGCAAAAGTGTGGCAGCTGGAC 477
Db 519 GAGGCCACACTGAATGACAGTGGCACCTTACCACCTGNCAGGGGTATCTTTAGGCAGGTGAA 578
Qy 478 TATGAGTCTGAGCCCTTCAACATTTACTTGTATAAAGCT 516
Db 579 TATGAATCTGACAAATTCAGAAATTCGTGTAGTAAAGCT 617

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Job time : 2359.62 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:4:29 ; Search time 2573.46 Seconds
(without alignments)
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Title: US-10-763-400-10
Perfect score: 591
Sequence: 1 atgctctgcatgaatc.....acattactgtaataaaagct 591

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
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- 25: em.ro.*
- 26: em.sts.*
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- 34: em.htg_pln.*
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- 37: em.htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	591	100.0	591	6	AR175486	AR175486 Sequence
2	591	100.0	591	6	AX074293	AX074293 Sequence
3	591	100.0	591	6	AX074295	AX074295 Sequence
4	591	100.0	713	6	E07699	E07699 cDNA encodi
5	591	100.0	773	6	AR219964	AR219964 Sequence
6	591	100.0	774	6	AR175481	AR175481 Sequence
7	591	100.0	774	6	AR175482	AR175482 Sequence
8	591	100.0	1068	6	A21606	A21606 human PC ep
9	591	100.0	1068	6	BD264325	BD264325 Recombina
10	591	100.0	1068	6	AX026808	AX026808 Sequence
11	591	100.0	1081	9	HUMMCTAA	J03605 Human mast
12	591	100.0	1102	9	BC005912	BC005912 Homo sapi
13	591	100.0	1106	9	BC015195	BC015195 Homo sapi
14	591	100.0	1174	6	AR123794	AR123794 Sequence
15	591	100.0	1198	6	AR175479	AR175479 Sequence
16	591	100.0	1198	6	AR175480	AR175480 Sequence
17	591	100.0	1198	6	AX074287	AX074287 Sequence
18	591	100.0	1198	6	AX074289	AX074289 Sequence
19	591	100.0	1198	6	AX101304	AX101304 Sequence
20	591	100.0	1198	6	AX335621	AX335621 Sequence
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24	591	100.0	2268	6	AX074303	AX074303 Sequence
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30	516	87.3	516	6	AR175487	AR175487 Sequence
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32	516	87.3	516	6	AX074298	AX074298 Sequence
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34	516	87.3	696	6	AX074290	AX074290 Sequence
35	516	87.3	696	6	AX074292	AX074292 Sequence
36	516	87.3	699	6	AR175483	AR175483 Sequence
37	516	87.3	1908	6	AX074315	AX074315 Sequence
38	516	87.3	1908	6	AX074317	AX074317 Sequence
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40	516	87.3	2193	6	AX074308	AX074308 Sequence
41	508	86.0	516	6	BD267592	BD267592 Crystalli
42	504.4	85.3	528	6	BD267591	BD267591 Crystalli
43	503.2	85.1	528	6	AX274971	AX274971 Sequence
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ALIGNMENTS

RESULT 1	AR175486	AR175486	591 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR175486	Sequence 10 from patent US 6309832.				
DEFINITION	AR175486	Sequence 10 from patent US 6309832.				
ACCESSION	AR175486	GI:17916785				
VERSION	AR175486.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 591)					
AUTHORS	Frank, G.R., Porter, J.P., Rushlow, K.E. and Wasson, D.L.					
TITLE	Method to detect Ige					
JOURNAL	Patent: US 6309832-A 10 30-OCT-2001;					
FEATURES	Location/Qualifiers					

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ORIGIN
Query Match 100.0%; Score 591; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.2e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGTCTCCTTCAGGCTCTGCTGAG 360
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Db 361 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGTGGTGGTGGTGGAGAACTGGGATGTG 420
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Db 421 TACAAGTGATCTATTATTAAGGATGGTGAAGTCTCAAGTACTGTGATGAGAACCAAC 480
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
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RESULT 2
AX074293
LOCUS AX074293 591 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 7 from Patent WO0104310.
ACCESSION AX074293
VERSION AX074293.1 GI:12710480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
1 Weber, E.R., Wood, K.V. and Hall, M.P.
AUTHORS Pc epsilon receptor-luminescence inducing protein chimeric nucleic
TITLE acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 7 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
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ORIGIN
Query Match 100.0%; Score 591; DB 6; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.2e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCTCCTGCCATGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTGGCTCCA 60
Db 1 ATGGCTCCTGCCATGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTGGCTCCA 60
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCCTCCTTGAACCCCTCCATGAATAGA 120
Db 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCCTCCTTGAACCCCTCCATGAATAGA 120
QY 121 ATATTTAAGGAGAGAAATGTGACTCTTACATGTATGGGAACAATTTCTTTGAAGTCAGT 180
Db 121 ATATTTAAGGAGAGAAATGTGACTCTTACATGTATGGGAACAATTTCTTTGAAGTCAGT 180
QY 181 TCCACCAAAATGGTTCACAAATGGCAGCCTTTTCCAGAAAGACACAAATTCAGATTGCAATATT 240
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QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTGAGCACAACAAGTTAATGAG 300
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QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGTCTCCTTCAGGCTCTGCTGAG 360
Db 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGTCTCCTTCAGGCTCTGCTGAG 360
QY 361 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGTGGTGGTGGTGGAGAACTGGGATGTG 420
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Db 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
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RESULT 3
AX074295/c
LOCUS AX074295 591 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 9 from Patent WO0104310.
ACCESSION AX074295
VERSION AX074295.1 GI:12710482
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
1 Weber, E.R., Wood, K.V. and Hall, M.P.
AUTHORS Pc epsilon receptor-luminescence inducing protein chimeric nucleic
TITLE acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 9 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)

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PC	C12N15/13	C12N5/10	C12P21/02			
CC	strandedness:	Double;				
CC	topology:	Linear;				
CC	hypothetical:	No;				
CC	anti-sense:	No;				
PH	Key		Location/Qualifiers			
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	Best Local Similarity	100.0%;	Pred. No. 3.3e-174;			
	Matches 591;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Qy	61	GATGGCGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTTGAAACCTCCATCGAATAGA	120			
Dd	180	GATGGCGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTTGAAACCTCCATCGAATAGA	239			
Qy	121	ATATTTAAAGGAGAGAAATGTACTCTTACATGTAATGGGAACAATTTCTTTCAAGTCAAGT	180			
Dd	240	ATATTTAAAGGAGAGAAATGTACTCTTACATGTAATGGGAACAATTTCTTTCAAGTCAAGT	299			
Qy	181	TCCACCAAAATGGTTCCACAATGGCAGCCCTTTCAGAAAGACACAAATTCAGTTTGAATATT	240			
Dd	300	TCCACCAAAATGGTTCCACAATGGCAGCCCTTTCAGAAAGACACAAATTCAGTTTGAATATT	359			
Qy	241	GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGCACCAACAAGTTAATGAG	300			
Dd	360	GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGCACCAACAAGTTAATGAG	419			
Qy	301	AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCCCTCTGCTGAG	360			
Dd	420	AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCCCTCTGCTGAG	479			
Qy	361	GTGGTGATGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTTGAGGAACCTGGGATGTG	420			
Dd	480	GTGGTGATGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTTGAGGAACCTGGGATGTG	539			
Qy	421	TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGGTATGAGAACCCACAAC	480			
Dd	540	TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGGTATGAGAACCCACAAC	599			
Qy	481	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTCTACGGCGCAAGTG	540			
Dd	600	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAAACCTTACTCTACGGCGCAAGTG	659			
Qy	541	TGGCAGCTGCAATGAGTCTGAGCCCTCAACATTACTGTATTAARAGCT	591			
Dd	660	TGGCAGCTGCAATGAGTCTGAGCCCTCAACATTACTGTATTAARAGCT	710			
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AR219964	DEFINITION	Sequence 6 from patent US 6423512.				
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Best Local Similarity	100.0%; Pred. No. 3.2e-174;
Matches 591; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGCGTCTCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTCTTTCGCTCCA 60
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QY	61 GATGCGGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
Db	531 GATGCGGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 472
QY	121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAGCAATTTCTTTGAAGTCAGT 180
Db	471 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAGCAATTTCTTTGAAGTCAGT 412
QY	181 TCCACCAAAATGGTTTCCAAATGGCAGCCCTTTTCAGAAAGAGACAAATTCGAATATT 240
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QY	241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAATGTGACACCAACCAAGTTAATGAG 300
Db	351 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAATGTGACACCAACCAAGTTAATGAG 292
QY	301 AGTGAACCTGTCTACTCTGGAAGTCTTCAAGTGAAGTGGTCTCTTTCAGGCGCTCTGCTGAG 360
Db	291 AGTGAACCTGTCTACTCTGGAAGTCTTCAAGTGAAGTGGTCTCTTTCAGGCGCTCTGCTGAG 232
QY	361 GTGTGTATGAGGGCGAGCCCTCTTTCCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
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QY	421 TACAAGGTGATCTATTATTAAGAGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
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QY	481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 540
Db	111 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 52
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E07699	713 bp RNA linear PAT 29-SEP-1997
LOCUS	CDNA encoding human soluble Fc epsilon RI alpha chain.
DEFINITION	E07699
ACCESSION	E07699.1 GI:2175833
VERSION	JP 1994169776-A/1.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 713)
AUTHORS	Ra,T., Naito,Y. and Hirama,M.
TITLE	PRODUCTION OF SOLUBLE HUMAN FcEPSILONRIALPHA CHAIN
JOURNAL	Patent: JP 1994169776-A 1 21-JUN-1994;
COMMENT	RA TOMOYASU, GREEN CROSS CORP:THE OS Homo sapiens (human) PN JP 1994169776-A/1 PD 21-JUN-1994 PF 29-JUL-1993 JP 92P 229227 PR 04-AUG-1992 JP 92P 229227

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SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 773)
AUTHORS      Digan, M.E., Lake, P. and Gram, H.
TITLE        Fusion polypeptides
JOURNAL      Patent: US 6423152-A 6 23-JUL-2002;
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACTCCATGGAATAGA 120
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QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
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DEFINITION   Sequence 5 from patent US 6309832.
ACCESSION    AR175482
VERSION       AR175482.1 GI:17916781
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 774)
AUTHORS      Frank, G.R., Porter, J.P., Rushlow, K.E. and Wassom, D.L.
TITLE        Method to detect Ige
JOURNAL      Patent: US 6309832-A 5 30-OCT-2001;
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Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCTCCTGCGCATGGAATCCCTCTACTCTACTGTGTGAGCTTACTGTCTTGGCTCCA 60

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DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACTCCATGGAATAGA 120

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DB 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTGTGTACGGGCAAGTG 540

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
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RESULT 6
LOCUS        AR175481
DEFINITION   Sequence 4 from patent US 6309832.
ACCESSION    AR175481
VERSION       AR175481.1 GI:17916780
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 774)
AUTHORS      Frank, G.R., Porter, J.P., Rushlow, K.E. and Wassom, D.L.
TITLE        Method to detect Ige

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ORIGIN

Query Match 100.0%; Score 591; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
DB 100 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 159
QY 121 ATATTAAAGGAGAGATGTGACTCTTACATGTAATGGAAACAATTTCTTTGAAGTCAGT 180
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DB 580 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 630

RESULT 9

BD264325 1068 bp DNA linear PAT 17-JUL-2003
Recombinant soluble Fc receptors.
BD264325
BD264325.1 GI:33074093
JP 2002531086-A/8.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1068)
AUTHORS
Sondermann, P., Huber, R. and Jakob, U.
TITLE
Recombinant soluble Fc receptors
JOURNAL
Patent: JP 2002531086-A 8 24-SEP-2002;
MAX PLANCK GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV
COMMENT
OS Homo sapiens (human)
PN JP 2002531086-A/8
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585398
PR 03-DEC-1998 EP 98122969.3

Best Local Similarity 100.0%; Pred. No. 3.4e-174;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCCTCCCA 60
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DB 714 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 655
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QY 541 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
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A21606 1068 bp DNA linear PAT 21-JUL-1994
LOCUS human Fc epsilon RI1a.
DEFINITION human Fc epsilon RI1a.
ACCESSION A21606
VERSION A21606.1 GI:579605
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1068)
AUTHORS
TITLE
HYBRID Fc RECEPTOR MOLECULES
JOURNAL Patent: WO 9106570-A 29 16-MAY-1991;
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/db_xref="SWISS-PROT:P12319"

PI PETER SONDERMANN, ROBERT HUBER, UWE JAKOB
 PC C12N15/09, A61K38/00, A61K45/00, A61P19/02, A61P29/00, A61P31/18,
 A61P35/00,
 PC A61P37/02, A61P37/08, C07K14/735, C12N1/21, G01N33/53, G01N33/53//
 PC (C12N1/21, C12N1/19), C12N15/00, A61K37/02
 CC Description of Artificial Sequence: Primer
 PH Key Location/Qualifiers
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 FT /organism='Homo sapiens (human)'.
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 Best Local Similarity 100.0%; Pred. No. 3.7e-174;
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 Db 40 ATGGCTCTCCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCTGCTCCA 99
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 LOCUS
 DEFINITION
 AX026808 Sequence 14 from Patent EPI006183.
 AX026808.1 GI:10187941
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 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1

AUTHORS
 TITLE
 JOURNAL
 RECOMBINANT SOLUBLE FC RECEPTORS
 PATENT: EP 1006183-A 14 07-JUN-2000;
 MAX PLANCK GSELLSCHAFT (DE)
 LOCATION/QUALIFIERS
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 Best Local Similarity 100.0%; Pred. No. 3.7e-174;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCTCTCCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCTGCTCCA 60
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 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGA 120
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 Db 340 AGTGAACCTGTGACTGGAAGTCTTCACTGAGTGGCTCTTCCAGGCTCTGCTGAG 399
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 Db 460 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCAAGTCTGATGAGACCAACAC 519
 QY 481 ATCTCCATTACAAATGCCACAGTTCAGAGACAGTGGAACTTACTGTACGGGCAAGGTG 540
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 QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
 Db 580 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 630

RESULT 11
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 LOCUS
 DEFINITION
 HUMC1A Human mast cell IgE receptor alpha-chain.
 J03605
 VERSION
 J03605.1 GI:187449
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1081)
 AUTHORS
 Shimizu, A., Tepler, I., Benfey, P.N., Berenstein, E.H.,
 Siraganian, R.P., and Leder, P.
 Human and rat mast cell high-affinity immunoglobulin E receptors:
 characterization of putative alpha-chain gene products
 Proc. Natl. Acad. Sci. U.S.A. 85 (6), 1907-1911 (1988)

88158102 2964640 MEDLINE PUBMED COMMENT	Original source text: Human mast cell line KUB12, cDNA to mRNA, clone PAS-h-IgER-110B. Computer-readable copy of sequence in [1] kindly provided by P.Leder, 08-FEB-1988. FEATURES Location/Qualifiers	DEFINITION
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Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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DB 35	ATGCTCTGCGATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCGCTCCA 94	
QY 61	GATGGCGTGTAGCAGTCCCTCAGAACCTAAGCTCTCTTGAACCTCCATGGAATGA 120	
DB 95	GATGGCGTGTAGCAGTCCCTCAGAACCTAAGCTCTCTTGAACCTCCATGGAATGA 154	
QY 121	ATATTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180	
DB 155	ATATTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 214	
QY 191	TCCACCAATGGTTCCACATGGCGAGCTTTTCAGAGAGACAAATTCAGTTTCAATATT 240	
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DB 330 AGTGAACCTGTGTACTGGAAGTCTTCAAGTGTGCTGCTCTTCAGGCCCTCTGCTGAG 389
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RESULT 13
BC015195
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DEFINITION
Homo sapiens Fc fragment of IgE, high affinity I, receptor for;
alpha polypeptide, mRNA (cdna clone MGC:14717 IMAGE:4251469),
complete cds.
ACCESSION
BC015195

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VERSION BC015195.1 GI:15929529
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1106)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,F.S., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,M., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahney,J., Helton,E., Kettaman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smillius,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
MEDLINE
12477932
2 (bases 1 to 1106)
Strausberg,R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Series: IRAL Plate: 21 Row: a Column: 14
This clone was selected for full length sequencing because it
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identity to protein.
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Db |||
Qy 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 697
Db |||

Search completed: October 10, 2004, 16:11:56
Job time : 2574.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 52.2483 Seconds
(without alignments)
6277.259 Million cell updates/sec

Title: US-10-763-400-10
Perfect score: 591
Sequence: 1 atggctctgcaatgaac.....acattactgtaataaaagct 591

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCFUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591	100.0	591	2	US-08-756-387B-10
2	591	100.0	591	2	US-09-285-873-10
3	591	100.0	591	4	US-09-944-277A-10
4	591	100.0	713	2	US-08-238-027-3
5	591	100.0	773	4	US-08-897-956A-6
6	591	100.0	774	2	US-08-756-387B-4
7	591	100.0	774	2	US-08-756-387B-5
8	591	100.0	774	4	US-09-285-873-4
9	591	100.0	774	4	US-09-285-873-5
10	591	100.0	774	4	US-09-944-277A-4
11	591	100.0	774	4	US-09-944-277A-5
12	591	100.0	1174	1	US-07-869-933-10
13	591	100.0	1174	3	US-09-103-663-10
14	591	100.0	1198	2	US-08-756-387B-1
15	591	100.0	1198	2	US-08-756-387B-3
16	591	100.0	1198	4	US-09-285-873-1
17	591	100.0	1198	4	US-09-285-873-3
18	591	100.0	1198	4	US-09-944-277A-1
19	591	100.0	1198	4	US-09-944-277A-3
20	591	100.0	2955	4	US-08-897-956A-4
21	589.4	99.7	591	3	US-08-788-954-1
22	516	87.3	516	2	US-08-756-387B-12
23	516	87.3	516	4	US-09-285-873-12
24	516	87.3	516	4	US-09-944-277A-12
25	516	87.3	699	2	US-08-756-387B-7
26	516	87.3	699	4	US-09-285-873-7
27	516	87.3	699	4	US-09-944-277A-7

28	329.8	55.8	603	3	US-09-015-734-11	Sequence 11, Appl
29	329.8	55.8	603	4	US-09-515-311-11	Sequence 11, Appl
30	329.8	55.8	765	3	US-09-015-734-4	Sequence 4, Appl
31	329.8	55.8	765	3	US-09-015-734-5	Sequence 5, Appl
32	329.8	55.8	765	4	US-09-515-311-4	Sequence 4, Appl
33	329.8	55.8	765	4	US-09-515-311-5	Sequence 5, Appl
34	329.8	55.8	1015	3	US-09-015-734-1	Sequence 1, Appl
35	329.8	55.8	1015	3	US-09-015-734-3	Sequence 3, Appl
36	329.8	55.8	1015	4	US-09-515-311-1	Sequence 1, Appl
37	329.8	55.8	1015	4	US-09-515-311-3	Sequence 3, Appl
38	302.8	51.2	597	2	US-08-768-964-11	Sequence 11, Appl
39	302.8	51.2	597	2	US-08-768-964-16	Sequence 16, Appl
40	302.8	51.2	597	3	US-09-005-299-11	Sequence 11, Appl
41	302.8	51.2	597	3	US-09-005-299-16	Sequence 16, Appl
42	302.8	51.2	597	3	US-09-515-431-11	Sequence 11, Appl
43	302.8	51.2	597	3	US-09-515-431-16	Sequence 16, Appl
44	302.8	51.2	789	2	US-08-768-964-4	Sequence 4, Appl
45	302.8	51.2	789	2	US-08-768-964-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-756-387B-10
; Sequence 10, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/494-9505
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..591
US-08-756-387B-10
Query Match 100.0%; Score 591; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.8e-186; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 0

;; TITLE OF INVENTION: Method to Detect Ige
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carol Talkington Verser, Ph.D.
;;
;; STREET: 1825 Sharp Point Drive
;; CITY: Fort Collins
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80525
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Wordperfect for Windows, Version 7.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/944,277A
;; FILING DATE: 30-Aug-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/285,873
;; FILING DATE: 1999-03-31
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Verser, Carol Talkington
;; REGISTRATION NUMBER: 37,459
;; REFERENCE/DOCKET NUMBER: DI-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 970/493-7272
;; TELEFAX: 970/484-9505
;;
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..591
;; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 100.0%; Score 591; DB 4; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.8e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCTCGTCCCA 60
DB 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTCTCGTCCCA 60

QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGA 120
DB 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGA 120

QY 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGACAAATTTCTTTGAATCAGT 180
DB 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGACAAATTTCTTTGAATCAGT 180

QY 181 TCCACCAATGGTTCACCAATGGCGCTTTTCAAGAGAGACAAATTTCAAGTTGAATATT 240
DB 181 TCCACCAATGGTTCACCAATGGCGCTTTTCAAGAGAGACAAATTTCAAGTTGAATATT 240

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATGAG 300
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATGAG 300

QY 301 AGTGAACCTGTGTACTCGAAGTCTTTCAGTGACTGGCTGCTCCCTTCAGGCTCTGCTGAG 360
DB 301 AGTGAACCTGTGTACTCGAAGTCTTTCAGTGACTGGCTGCTCCCTTCAGGCTCTGCTGAG 360

QY 361 GTGGTGTAGGAGGCGCCGCCCTCTTCTCAGTGCCCATGCTTGGAGAACTGGGATGTG 420
DB 361 GTGGTGTAGGAGGCGCCGCCCTCTTCTCAGTGCCCATGCTTGGAGAACTGGGATGTG 420

QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480
DB 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480

QY 481 ATCTCCATTACAAATGCCACAGTTGACAGACAGTGGAACTTACTGTACGGGCAAGTG 540
DB 481 ATCTCCATTACAAATGCCACAGTTGACAGACAGTGGAACTTACTGTACGGGCAAGTG 540

QY 541 TGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
DB 541 TGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTGTAAATAAAGCT 591

RESULT 4
US-08-238-027-3
; Sequence 3, Application US/08238027
; Patent No. 5874404
; GENERAL INFORMATION:
; APPLICANT: RA, CHISEI
; APPLICANT: NAITO, KOJI
; APPLICANT: HIRAMA, MINORU
; APPLICANT: OKUMURA, KO
; TITLE OF INVENTION: ANTIALLERGIC COMPOSITION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVENUE
; CITY: N.W.
; STATE: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,027
; FILING DATE: 03-MAY-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-229227
; FILING DATE: 04-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-213002
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-270513
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-270514
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-270515
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-208217
; FILING DATE: 29-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-197341
; FILING DATE: 09-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-251605
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-251606
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-251608
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-261355

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; FILING DATE: 19-OCT-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-264802
; FILING DATE: 22-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 120..713
; IDENTIFICATION METHOD: by similarity with known
; IDENTIFICATION METHOD: sequence or to an established consensus
US-08-238-027-3

Query Match 100.0%; Score 591; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 7.6e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTTCCTCGCTCCA 60
DB 120 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGTAGCTTACTGTTCCTCGCTCCA 179

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGAATAGA 120
DB 180 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGAATAGA 239

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGGAACAATTTCTTGAAGTCAGT 180
DB 240 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGGAACAATTTCTTGAAGTCAGT 299

QY 181 TCCACCAATGGTTCACCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 300 TCCACCAATGGTTCACCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATT 359

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300
DB 360 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 419

QY 301 AGTGAACTGTGTACCTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGGCTCTGCTGAG 360
DB 420 AGTGAACTGTGTACCTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGGCTCTGCTGAG 479

QY 361 GTGGTGATGGAGGGGCGACCCCTCTTCTCAGTGGCCATGGTTGGAGAACTGGGATGTG 420
DB 480 GTGGTGATGGAGGGGCGACCCCTCTTCTCAGTGGCCATGGTTGGAGAACTGGGATGTG 539

QY 421 TACAAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTCTCAAGTCTGATGAGAACCAAC 480
DB 540 TACAAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTCTCAAGTCTGATGAGAACCAAC 599

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
DB 600 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 659

QY 541 TGGCAGCTGGACTGATGACTGTAGGCTTGGAGCCCTCAACATTACTGTATAAAGCT 591
DB 660 TGGCAGCTGGACTGATGACTGTAGGCTTGGAGCCCTCAACATTACTGTATAAAGCT 710
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RESULT 5
US-08-997-956A-6
; Sequence 6, Application US/08997956A
; Patent No. 6423512
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; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/997,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-997-956A-6

Query Match 100.0%; Score 591; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 8e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCCTCGCTCCA 60
DB 1 ATGGCTCTCGCATGGAAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCCTCGCTCCA 60

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGAATAGA 120
DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTCTTGAACCTCCATGAATAGA 120

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGGAACAATTTCTTGAAGTCAGT 180
DB 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGGAACAATTTCTTGAAGTCAGT 180

QY 181 TCCACCAATGGTTCACCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 181 TCCACCAATGGTTCACCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGACCAACCAAGTTAATGAG 300

QY 301 AGTGAACTGTGTACCTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGGCTCTGCTGAG 360
DB 301 AGTGAACTGTGTACCTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGGCTCTGCTGAG 360

QY 361 GTGGTGATGGAGGGGCGACCCCTCTTCTCAGTGGCCATGGTTGGAGAACTGGGATGTG 420
DB 361 GTGGTGATGGAGGGGCGACCCCTCTTCTCAGTGGCCATGGTTGGAGAACTGGGATGTG 420

QY 421 TACAAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTCTCAAGTCTGATGAGAACCAAC 480
DB 421 TACAAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTCTCAAGTCTGATGAGAACCAAC 480

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
DB 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540

QY 541 TGGCAGCTGGACTGATGACTGTAGGCTTGGAGCCCTCAACATTACTGTATAAAGCT 591
DB 541 TGGCAGCTGGACTGATGACTGTAGGCTTGGAGCCCTCAACATTACTGTATAAAGCT 591
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RESULT 6
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
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Db	421	TACAAGGTGA	CTATTATAAAGGATGGTCAAGCTCTCAAGTACTTGTTATGAGAACACCAAC	480
Qy	481	ATCTCCATTACA	AAATGCCACAGTTCGAACACAGTGGAACTTACTACTGTACGGGCAAAGTG	540
Db	481	ATCTCCATTACA	AATGCCACAGTTCGAACACAGTGGAACTTACTACTGTACGGGCAAAGTG	540
Qy	541	TGGCAGCTGG	ACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAAAGCT	591
Db	541	TGGCAGCTGG	ACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAAAGCT	591
 RESULT 7 US-08-756-387B-5/c ; Sequence 5, Application US/08756387B ; Patent No.. 5945294 ; GENERAL INFORMATION: ; APPLICANT: Wassom, Donald L. ; APPLICANT: Frank, Glenn R. ; APPLICANT: Porter, James P. ; APPLICANT: Rushlow, Keith E. ; APPLICANT: Wassom, Donald L. ; TITLE OF INVENTION: Method to Detect Ige ; NUMBER OF SEQUENCES: 13 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Carol Talkington Verser, Ph.D. ; ADDRESSEE: Heska Corporation ; STREET: 1825 Sharp Point Drive ; CITY: Fort Collins ; STATE: Colorado ; COUNTRY: USA ; ZIP: 80525 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: Windows 95 ; SOFTWARE: WordPerfect for Windows, Version 7.0 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/756,387B ; FILING DATE: NO. 5945294ember 26, 1996 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: Verser, Carol Talkington ; REGISTRATION NUMBER: 37,459 ; REFERENCE/DOCKET NUMBER: DI-1 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 970/493-7272 ; TELEFAX: 970/484-9505 ; INFORMATION FOR SEQ ID NO: 5: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 774 nucleotides ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: cdna ; US-08-756-387B-5				
 Query Match 100.0%; Score 591; DB 2; Length 774; Best Local Similarity 100.0%; Pred. No. 8e-186; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
Qy	1	ATGGCTCTCGCAT	GGAATCCCCTACTCTACTCTGTGTAGCCTTACTGTCTTCGCTCCA	60
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Qy	61	GATGGCGTGTAG	CAGTCCCTCAGAACCTTAAGSTCTCTTGAAACCTCCATGGAATAGA	120
Db	714	GATGGCGTGTAG	CAGTCCCTCAGAACCTTAAGSTCTCTTGAAACCTCCATGGAATAGA	655
Qy	121	ATATTTAAAGG	AGAGATGTGACTCTTACATGTAATGGGAACAAATTCITTTGAAGTCAGT	180
Db	654	ATATTTAAAGG	AGAGATGTGACTCTTACATGTAATGGGAACAAATTCITTTGAAGTCAGT	595
Qy	181	TCCACCAAAAT	GGTTTCCCAATGGCAGCCTTTACAGAGACAAATTCAGATTTGAATATT	240

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Db 594 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAGAGACAAATCAAGTTTGAATATT 535
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAAGTTAATGAG 300
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAAGTTAATGAG 475
QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGSCCTCTGCTGAG 360
Db 474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGSCCTCTGCTGAG 415
QY 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGGTGGAGGAACCTGGAGTGTG 420
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QY 421 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAGTACTGGTATGAGAACCAAC 480
Db 354 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAGTACTGGTATGAGAACCAAC 295
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540
Db 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 235
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
Db 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 184
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RESULT 8

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US-09-285-873-4
; Sequence 4, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285.873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: 1..774
US-09-285-873-4
Query Match
Best Local Similarity 100.0%; Score 591; DB 4; Length 774;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCTCCTGCCATGGAATCCCTACTACTCTGTGTAGCTTACTGTCTTTCGTCCTCA 60
Db 1 ATGGCTCCTGCCATGGAATCCCTACTACTCTGTGTAGCTTACTGTCTTTCGTCCTCA 60
QY 61 GATGGCGTGTAGCAGTCCCTCAGAACTTAAAGTCTCTTGAACCCCTCCATGGAATAGA 120
Db 61 GATGGCGTGTAGCAGTCCCTCAGAACTTAAAGTCTCTTGAACCCCTCCATGGAATAGA 120
QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTATCATGTAATGGAAACAATTTCTTGAAGTCA 180
Db 121 ATATTTAAAGGAGAGAAATGTGACTCTTATCATGTAATGGAAACAATTTCTTGAAGTCA 180
QY 181 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
Db 181 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATT 240
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAAGTTAATGAG 300
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAAGTTAATGAG 300
QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTTCAGTGGTGGAGGAACCTGGATGTG 360
Db 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTTCAGTGGTGGAGGAACCTGGATGTG 360
QY 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGGTGGAGGAACCTGGATGTG 420
Db 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGGTGGAGGAACCTGGATGTG 420
QY 421 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
Db 421 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540
Db 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
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RESULT 9

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US-09-285-873-5/c
; Sequence 5, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-285-873-5
;
; Query Match 100.0%; Score 591; DB 4; Length 774;
; Best Local Similarity 100.0%; Pred. No. 8e-186;
; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ATGGCTCTGCTGCAATGGAATCCCTTACTGTGTGTAGCTTACTGTCTTCTTCTGCTCCA 60
; DB 774 ATGGCTCTGCTGCAATGGAATCCCTTACTGTGTGTAGCTTACTGTCTTCTTCTGCTCCA 715
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; QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 120
; DB 714 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 655
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; QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
; DB 654 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595
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; QY 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAAAGACAAATTCAGATTTGAATATT 240
; DB 594 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAAAGACAAATTCAGATTTGAATATT 535
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; QY 241 GTGAATGCCAAATTTGAAGAGAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
; DB 534 GTGAATGCCAAATTTGAAGAGAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 475
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; QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTTCAAGGCTCTGCTGAG 360
; DB 474 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTTCAAGGCTCTGCTGAG 415
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; QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAAGTGGGATGTG 420
; DB 414 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGGAAGTGGGATGTG 355
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; QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 480
; DB 354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 295
;
; QY 481 ATCTCCATACAAATGCCACAGTTGAACAGAGTGAACCTACTACTGTACGGCAAGTG 540
; DB 294 ATCTCCATACAAATGCCACAGTTGAACAGAGTGAACCTACTACTGTACGGCAAGTG 235
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; QY 541 TGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
; DB 234 TGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 184
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; RESULT 10
; US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
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;
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-09-944-277A-4
;
; Query Match 100.0%; Score 591; DB 4; Length 774;
; Best Local Similarity 100.0%; Pred. No. 8e-186;
; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ATGGCTCTGCAATGGAATCCCTTACTGTGTGTAGCTTACTGTCTTCTTCTGCTCCA 60
; DB 1 ATGGCTCTGCAATGGAATCCCTTACTGTGTGTAGCTTACTGTCTTCTTCTGCTCCA 60
;
; QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 120
; DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 120
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; QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
; DB 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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; QY 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAAAGACAAATTCAGATTTGAATATT 240
; DB 181 TCCACCAATGGTTCACAAATGGCAGCTTTCAGAAAGACAAATTCAGATTTGAATATT 240
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; QY 241 GTCAATGCCAAATTTGAAGAGAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
; DB 241 GTCAATGCCAAATTTGAAGAGAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
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; QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTTCAAGGCTCTGCTGAG 360
; DB 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTTCAAGGCTCTGCTGAG 360
;

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QY 361 GTGGTGTAGAGGGCCAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTG 420
DB 361 GTGGTGTAGAGGGCCAGCCCTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTG 420
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
DB 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 540
DB 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 540
QY 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591
DB 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591

RESULT 11

US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. 6682894

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.
Porter, James P.
Rushlow, Keith E.
Wasson, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSER: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-944-277A-5

Query Match

Best Local Similarity 100.0%; Score 591; DB 4; Length 774;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCGCTCCA 60
DB 774 ATGGCTCTGCCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCGCTCCA 715

QY 61 GATGGCGGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCCTTGAACCCCTCCATGGAATAGA 120
DB 714 GATGGCGGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCCTTGAACCCCTCCATGGAATAGA 655
QY 121 ATATTTAAAGSAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 654 ATATTTAAAGSAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 595
QY 181 TCACACAAATGGTTCCACANTGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATT 240
DB 594 TCACACAAATGGTTCCACANTGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATATT 535
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
DB 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 475
QY 301 AGTGAACCTGTGTACCTGGAGTCTTTCAGTACTGGCTGCTCTTTCAGGCTCTGCTGAG 360
DB 474 AGTGAACCTGTGTACCTGGAGTCTTTCAGTACTGGCTGCTCTTTCAGGCTCTGCTGAG 415
QY 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
DB 414 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480
DB 354 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 295
QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 540
DB 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTG 235
QY 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591
DB 234 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 184

RESULT 12

US-07-869-933-10

; Sequence 10, Application US/07869933

; Patent No. 5770396

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933

FILING DATE: 19920416

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/154 NTHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 10:


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SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: NUCLEIC ACID
; ORGANISM: Homo sapiens
; FEATURE:
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 107..880
US-07-869-933-10

Query Match      100.0%; Score 591; DB 1; Length 1174;
Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTTGTTCCTTGGTCTCA 60
DB 107 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTTGTTCCTTGGTCTCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGA 120
DB 167 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGA 226

QY 121 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 227 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

QY 181 TCCACCAAAATGGTTCCCAATGGCAGCCTTTTCCAGAACGACAAATTCAGTTTGAATATT 240
DB 287 TCCACCAAAATGGTTCCCAATGGCAGCCTTTTCCAGAACGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACTGTGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 360
DB 407 AGTGAACCTGTGTACTGTGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 420
DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 526

QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 480
DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTGAAGACAGTGGAACTACTCTGTACGGGCAAGTG 540
DB 587 ATCTCCATTACAAATGCCACAGTGAAGACAGTGGAACTACTCTGTACGGGCAAGTG 646

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 697
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RESULT 13
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinect et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; FILE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
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; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(880)
US-09-103-663-10

Query Match      100.0%; Score 591; DB 3; Length 1174;
Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTTGTTCCTTGGTCTCA 60
DB 107 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTTGTTCCTTGGTCTCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGA 120
DB 167 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGA 226

QY 121 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
DB 227 ATATTTAAAGGAGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

QY 181 TCCACCAAAATGGTTCCCAATGGCAGCCTTTTCCAGAACGACAAATTCAGTTTGAATATT 240
DB 287 TCCACCAAAATGGTTCCCAATGGCAGCCTTTTCCAGAACGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACTGTGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 360
DB 407 AGTGAACCTGTGTACTGTGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 420
DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 526

QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 480
DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTGAAGACAGTGGAACTACTCTGTACGGGCAAGTG 540
DB 587 ATCTCCATTACAAATGCCACAGTGAAGACAGTGGAACTACTCTGTACGGGCAAGTG 646

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 697
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RESULT 14
US-08-756-387B-1
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: NO. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
;
US-08-756-387B-1

Query Match 100.0%; Score 591; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGCCATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTCTGCTCCA 60
Db 107 ATGGCTCTGCGCATGCCATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTCTGCTCCA 166

QY 61 GATGGCGTGTAGAGTCTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 120
Db 167 GATGGCGTGTAGAGTCTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 226

QY 121 ATATTAAAGGAGAGAAATGTAGCTTACATGTAAATGGGAACAATTTCTTGAAGTCAGT 180
Db 227 ATATTAAAGGAGAGAAATGTAGCTTACATGTAAATGGGAACAATTTCTTGAAGTCAGT 286

QY 181 TCCACCAAAATGGTTCCCAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
Db 287 TCCACCAAAATGGTTCCCAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAGTTAATGAG 300
Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGTAGTGGCTCTCTTTCAGGCTCTGCTGAG 360
Db 407 AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGTAGTGGCTCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGTAGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGATGTG 420
Db 467 GTGGTGTAGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGATGTG 526

QY 421 TACAGGTGTACTATTATTAAGATGGTGAAGCTCTCAAGTCTCAAGTCTGATGAGAACCAAC 480
Db 527 TACAGGTGTACTATTATTAAGATGGTGAAGCTCTCAAGTCTCAAGTCTGATGAGAACCAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTGTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG 540
Db 587 ATCTCCATTACAAATGCCACAGTGTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG 646

QY 541 TGGGAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAGCT 591
Db 647 TGGGAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTAAATAAGCT 697

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US-08-756-387B-3/c
; Sequence 3, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: NO. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
US-08-756-387B-3

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Query Match 100.0%; Score 591; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1092 ATGGCTCTGCGCATGCCATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTCTGCTCCA 1033

QY 61 GATGGCGTGTAGAGTCTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 120
Db 1032 GATGGCGTGTAGAGTCTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 973

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QY 181 TCCACCAAAATGGTTCCCAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
Db 912 TCCACCAAAATGGTTCCCAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 853

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAGTTAATGAG 300
Db 852 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACAGCCCAACAAGTTAATGAG 793

QY 301 AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGTAGTGGCTCTCTTTCAGGCTCTGCTGAG 360
Db 792 AGTGAACCTGTGTACTCTGAAAGTCTTTCAGTGTAGTGGCTCTCTTTCAGGCTCTGCTGAG 733

QY 361 GTGGTGTAGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420

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Db	672	TACAAGGTGATCTATTATATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC	613	
Qy	481	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTTACTACGGGCAAAAGTG	540	
Db	612	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTTACTACGGGCAAAAGTG	553	
Qy	541	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT	591	
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Job time : 53.2483 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:20:22 ; Search time 344.307 Seconds
(without alignments)
8701.874 Million cell updates/sec

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Perfect score: 591
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Gapop 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues
Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591	100.0	591	9	US-09-944-277A-10
2	591	100.0	774	9	US-09-944-277A-4
3	591	100.0	774	9	US-09-944-277A-5
4	591	100.0	898	13	US-10-236-392-27
5	591	100.0	1198	9	US-09-944-277A-1
6	591	100.0	1198	9	US-09-944-277A-3
7	591	100.0	1198	9	US-09-962-832-244
8	591	100.0	1198	17	US-10-775-169-141
9	516	87.3	516	9	US-09-944-277A-12
10	516	87.3	516	13	US-10-293-392-3
11	516	87.3	528	10	US-09-809-715-1
12	516	87.3	528	13	US-10-293-992-1
13	516	87.3	699	9	US-09-944-277A-7
14	503.2	85.1	528	10	US-09-809-715-3

15	347	58.7	757	13	US-10-236-392-29
16	329.8	55.8	603	16	US-10-434-817-11
17	329.8	55.8	765	16	US-10-434-817-4
18	329.8	55.8	765	16	US-10-434-817-5
19	329.8	55.8	1015	16	US-10-434-817-1
20	329.8	55.8	1015	16	US-10-434-817-3
21	298.6	50.5	708	16	US-10-434-817-6
22	298.6	50.5	708	16	US-10-434-817-8
23	168.6	28.5	2202	15	US-10-198-846-13731
24	167	28.3	765	15	US-10-027-736A-8
25	167	28.3	887	17	US-10-641-643-1287
26	165.4	28.0	887	16	US-10-191-997-124
27	165.4	28.0	887	17	US-10-641-643-1254
28	165.4	28.0	887	17	US-10-717-597-208
29	165.4	28.0	887	17	US-10-775-169-140
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32	162.2	27.4	1977	13	US-10-240-425-1268
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35	162.2	27.4	1977	13	US-10-775-169-35
36	159	26.9	765	15	US-10-027-736A-7
37	141.6	24.0	1318	12	US-10-152-319A-2037
38	141.6	24.0	1318	16	US-10-191-803-266
39	140	23.7	1341	16	US-10-388-934-244
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45	138	23.4	1074	15	US-10-027-736A-1

ALIGNMENTS

RESULT 1

US-09-944-277A-10
; Sequence 10, Application US/09944277A
; Patent No. US00030034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

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; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..591
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 100.0%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.6e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCCGCGCATGGAATCCCTACTCTACTGTGTAGAGCTTACTGTCTTCGCTCCA 60
Db 1 ATGGCTCCGCGCATGGAATCCCTACTCTACTGTGTAGAGCTTACTGTCTTCGCTCCA 60

QY 61 GATGGCGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 GATGGCGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120

QY 121 ATATTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 ATATTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 181 TCCACCAATGTTTCCCAATGCGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 TCCACCAATGTTTCCCAATGCGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

QY 241 GTGAATGCCAAATTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GTGAATGCCAAATTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 301 AGTGAACCTGTACTCTGGAAGTCTTCAAGTACTGCTGCTTCAAGGCTCTGCTGAG 360
Db 301 AGTGAACCTGTACTCTGGAAGTCTTCAAGTACTGCTGCTTCAAGGCTCTGCTGAG 360

QY 361 GTGGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GTGGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 421 TACAGAGTGTATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 TACAGAGTGTATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

QY 481 ATCTCCATTACAAATGCCACAGTGTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 ATCTCCATTACAAATGCCACAGTGTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 541 TGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
Db 541 TGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591

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RESULT 2

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US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation

```

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; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

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Query Match 100.0%; Score 591; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 4.3e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCCGCGCATGGAATCCCTACTCTACTGTGTAGAGCTTACTGTCTTCGCTCCA 60
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QY 61 GATGGCGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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Db 241 GTGAATGCCAAATTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 301 AGTGAACCTGTACTCTGGAAGTCTTCAAGTACTGCTGCTTCAAGGCTCTGCTGAG 360
Db 301 AGTGAACCTGTACTCTGGAAGTCTTCAAGTACTGCTGCTTCAAGGCTCTGCTGAG 360

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Db 361 GTGGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

QY 421 TACAGAGTGTATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
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QY 481 ATCTCCATTACAAATGCCAGTTGAAGACAGTGGAACTTACTACTGTAGCGGCAAGTG 540
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Db 541 TGGCAGTGGACTATGAGTGTGAGCCCTCAACATTAATCTGTATATAAAGCT 591

RESULT 3

US-09-944-277A-5/c
; Sequence 5, Application US/09944277A

; Patent No. US20020034771A1

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

Porter, James P.

Rushlow, Keith E.

Wassom, Donald L.

TITLE OF INVENTION: Method to Detect IgE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-944-277A-5

Query Match 100.0%; Score 591; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 4.3e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 774 ATGGCTCTGCGATCGAATCCCTTACTCTACTGTGTAGCCTTACTGTCTTCTGCTCCA 715
QY 61 GATGGCGTTGTAGCAGTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
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Db 534 GTGAATGCCAAATTTTGAAGACAGTGGGAATAACAAATGTACGACCAACAAGTTTAATGAG 475
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Db 474 AGTGAACCTGTGTACCTGGAAAGTCTTTCAGTGTGCTGCTCTTCAGGCGCTCTGCTGAG 415
QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
Db 414 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 355
QY 421 TACAAGGTGATCTATATTAAGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAC 480
Db 354 TACAAGGTGATCTATATTAAGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAC 295
QY 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
Db 294 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 235
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Db 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 184

RESULT 4

US-10-236-392-27

; Sequence 27, Application US/10236392

; Publication No. US20040067490A1

GENERAL INFORMATION:

APPLICANT: Anderson, David W

APPLICANT: Boldog, Ferenc L

APPLICANT: Burgess, Catherine, E

APPLICANT: Casman, Stacie J

APPLICANT: Catterton, Elina

APPLICANT: Chapoval, Andrei

APPLICANT: Crabtree, Julie

APPLICANT: Edinger, Shlomit, R

APPLICANT: Ellerman, Karen

APPLICANT: Gerlach, Valerie

APPLICANT: Gorman, Linda

APPLICANT: Grosse, William M

APPLICANT: Gusev, Vladimir

APPLICANT: Kekuda, Ramesh

APPLICANT: LaRocheville, William J

APPLICANT: Li, Li

APPLICANT: MacDougall, John R

APPLICANT: Malyankar, Uriel M

APPLICANT: Miller, Charles E

APPLICANT: Millet, Isabelle

APPLICANT: Padigaru, Muralidhara

APPLICANT: Patturajan, Meera

APPLICANT: Pena, Carol A

APPLICANT: Peyman, John A

APPLICANT: Rastelli, Luca

APPLICANT: Reiger, Daniel K

APPLICANT: Rothenberg, Mark E

APPLICANT: Shenoy, Suresh

APPLICANT: Shinkets, Richard A

APPLICANT: Smithson, Glennda

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-442A

CURRENT APPLICATION NUMBER: US/10/236,392

CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US09/540,763

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: US60/390,155

PRIOR FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US09/635,949

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; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 27
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(797)
US-10-236-392-27

Query Match      100.0%; Score 591; DB 13; Length 898;
Best Local Similarity 100.0%; Pred. No. 4.8e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGGCATGAATCCCTACTCTACTGTGTGTAGCTTACTTCTTTCGCTCCA 60
DB 26 ATGGCTCTGGCATGAATCCCTACTCTACTGTGTGTAGCTTACTTCTTTCGCTCCA 85

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 120
DB 86 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 145

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGAACAATTTCTTTGAAGTCAGT 180
DB 146 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGAACAATTTCTTTGAAGTCAGT 205

QY 181 TCCACCAATGTCTCCAAATGCGAGCTTTTACAGAGAGACAAATTCAGTTTGAATATT 240
DB 206 TCCACCAATGTCTCCAAATGCGAGCTTTTACAGAGAGACAAATTCAGTTTGAATATT 265

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAGTTAATGAG 300
DB 266 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAGTTAATGAG 325

QY 301 AGTGAACCTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTCAGGCTCTGCTGAG 360
DB 326 AGTGAACCTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTCAGGCTCTGCTGAG 385

QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGSCCATGGTGGAGGAATCGGATGTG 420
DB 386 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGSCCATGGTGGAGGAATCGGATGTG 445

QY 421 TACAGGTGATCTATTATTAAGATGGTGAAGTCTCAAGTACTGATGAGAACCAAC 480
DB 446 TACAGGTGATCTATTATTAAGATGGTGAAGTCTCAAGTACTGATGAGAACCAAC 505

QY 481 ATCTCCATTACAAATGCCACAGTTGAACACAGTGAACCTACTACTGTACGGGCAAGTG 540
DB 506 ATCTCCATTACAAATGCCACAGTTGAACACAGTGAACCTACTACTGTACGGGCAAGTG 565

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
DB 566 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 616

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RESULT 5

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US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match      100.0%; Score 591; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 60
DB 107 ATGGCTCTCGCATGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 120
DB 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGAATAGA 226

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGAACAATTTCTTTGAAGTCAGT 180
DB 227 ATATTAAAGGAGAGAAATGTGACTCTTACATGTATATGGAACAATTTCTTTGAAGTCAGT 286

QY 181 TCCACCAATGTCTCAATGCGAGCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 240
DB 287 TCCACCAATGTCTCAATGCGAGCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAGTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAGTTAATGAG 406

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QY 301 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGCTGCTCTTCAAGGCTCTGCTGAG 360
Db 407 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGCTGCTCTTCAAGGCTCTGCTGAG 466
QY 361 GTGGTGTAGAGGGCCAGCCCTCTTCCCTCAGGTGCCATGTTGGAGGAACCTGGGATGTG 420
Db 467 GTGGTGTAGAGGGCCAGCCCTCTTCCCTCAGGTGCCATGTTGGAGGAACCTGGGATGTG 526
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 480
Db 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 586
QY 481 ATCTCCATTACAATGCCACAGTGAAGAGTGAAGCTCTCAAGTACTGTTATGAGAACCAAGT 540
Db 587 ATCTCCATTACAATGCCACAGTGAAGAGTGAAGCTCTCAAGTACTGTTATGAGAACCAAGT 646
QY 541 TGGCAGCTGACTATGATCTCTGAGCCCTCAACATTAATTAATAAAGCT 591
Db 647 TGGCAGCTGACTATGATCTCTGAGCCCTCAACATTAATTAATAAAGCT 697

RESULT 6

US-09-944-277A-3/C
; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 100.0%; Score 591; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTTACTCTACTGTGTGTAGCTTTACTGTCTTTCGCTCCA 60
Db 1092 ATGGCTCTGCGCATGGAATCCCTTACTCTACTGTGTGTAGCTTTACTGTCTTTCGCTCCA 1033
QY 61 GATGCGGTGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
Db 1032 GATGCGGTGTGTAGCAGTCCCTCAGAAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 973
QY 121 ATATTTAAAGAGAGAGATGTGACTTTCATGTATTAATGGGACAAATTTCTTTGAAAGTCAGT 180
Db 972 ATATTTAAAGAGAGAGATGTGACTTTCATGTATTAATGGGACAAATTTCTTTGAAAGTCAGT 913
QY 181 TCCACCAATGGTTCACAAATGGCAGCCCTTTTCAAGAGAGACAAATTCAGTTTCAATATT 240
Db 912 TCCACCAATGGTTCACAAATGGCAGCCCTTTTCAAGAGAGACAAATTCAGTTTCAATATT 853
QY 241 GTGAATGCCAAATTTTGAAGACAGTGGAGAAATACAAATGTCAAGCACCACCAAGTTAATGAG 300
Db 852 GTGAATGCCAAATTTTGAAGACAGTGGAGAAATACAAATGTCAAGCACCACCAAGTTAATGAG 793
QY 301 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGCCCTCTGCTGAG 360
Db 792 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTCAAGCCCTCTGCTGAG 733
QY 361 GTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTG 420
Db 732 GTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTG 673
QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 480
Db 672 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAC 613
QY 481 ATCTCCATTACAATGCCACAGTTCGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540
Db 612 ATCTCCATTACAATGCCACAGTTCGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 553
QY 541 TGGCAGCTGACTATGATCTCTGAGCCCTCAACATTAATTAATAAAGCT 591
Db 552 TGGCAGCTGACTATGATCTCTGAGCCCTCAACATTAATTAATAAAGCT 502

RESULT 7

US-09-962-832-244
; Sequence 244, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-832-244

Query Match 100.0%; Score 591; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTTACTCTACTGTGTGTAGCTTTACTGTCTTTCGCTCCA 60
Db 107 ATGGCTCTGCGCATGGAATCCCTTACTCTACTGTGTGTAGCTTTACTGTCTTTCGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCTCCATGGAATAGA 120
 Db 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCTCCATGGAATAGA 226
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 180
 Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 286
 QY 181 TCACCAATGTTCCCAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
 Db 287 TCACCAATGTTCCCAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
 Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 406
 QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 360
 Db 407 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 466
 QY 361 GTGGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
 Db 467 GTGGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
 QY 421 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 480
 Db 527 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 586
 QY 481 ATCTCCATTACAAATGCCACAGTTCAGACAGTGAACCTACTACTGTACGGGCAAGTG 540
 Db 587 ATCTCCATTACAAATGCCACAGTTCAGACAGTGAACCTACTACTGTACGGGCAAGTG 646
 QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
 Db 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 697

RESULT 8
 US-10-775-169-141
 ; Sequence 141, Application US/10775169
 ; Publication No. US2004017543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Burczynski, Michael
 ; APPLICANT: Twine, Natalie
 ; APPLICANT: Dornier, Andrew
 ; APPLICANT: Trepicchio, William
 ; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
 ; FILE REFERENCE: AM101080 (031896-013000)
 ; CURRENT APPLICATION NUMBER: US/10/775,169
 ; CURRENT FILING DATE: 2004-02-11
 ; NUMBER OF SEQ ID NOS: 5278
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 141
 ; LENGTH: 1198
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-775-169-141

Query Match 100.0%; Score 591; DB 17; Length 1198;
 Best Local Similarity 100.0%; Pred. No. 5,7e-183;
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCAGTAACTCCCTACTACTGTGTGTAGCTTACTGTCTTCTGCTCCA 60
 Db 107 ATGGCTCTGCGCAGTAACTCCCTACTACTGTGTGTAGCTTACTGTCTTCTGCTCCA 166
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCTCCATGGAATAGA 120
 Db 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCTCCATGGAATAGA 226
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 180

Db 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 286
 QY 181 TCACCAATGTTCCCAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
 Db 287 TCACCAATGTTCCCAATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
 Db 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 406
 QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 360
 Db 407 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 466
 QY 361 GTGGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
 Db 467 GTGGTGATGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
 QY 421 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 480
 Db 527 TACAAGGTGATCTATTATTAAGAGTGGTGAAGCTCTCAAGTACTGTGATGAGAACCAAC 586
 QY 481 ATCTCCATTACAAATGCCACAGTTCAGACAGTGAACCTACTACTGTACGGGCAAGTG 540
 Db 587 ATCTCCATTACAAATGCCACAGTTCAGACAGTGAACCTACTACTGTACGGGCAAGTG 646
 QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
 Db 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 697

RESULT 9
 US-09-944-277A-12
 ; Sequence 12, Application US/09944277A
 ; Patent No. US20020034771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frank, Glenn R.
 ; Porter, James P.
 ; Rushlow, Keith E.
 ; Wassom, Donald L.
 ; TITLE OF INVENTION: Method to Detect Ige
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.
 ; STREET: 1825 Sharp Point Drive
 ; CITY: Fort Collins
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80525
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: WordPerfect for Windows, Version 7.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/944,277A
 ; FILING DATE: 30-Aug-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/285,873
 ; FILING DATE: 1999-03-31
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Verser, Carol Talkington
 ; REGISTRATION NUMBER: 37,459
 ; REFERENCE/DOCKET NUMBER: DI-1
 ; TELEPHONE: 970/493-7272
 ; TELEFAX: 970/484-9505
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 516 nucleotides
 ; TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

Query Match 87.3%; Score 516; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.5e-158;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCAGTGAATAGATATTTAAAGGAG 135
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCAGTGAATAGATATTTAAAGGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTTCACCAATGTTTC 195
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTTCACCAATGTTTC 120

QY 196 CACAATGGCAGCCTTTTCAAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 255
Db 121 CACAATGGCAGCCTTTTCAAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 180

QY 256 GAAGCAGTGGAGATACAAATGTGAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 315
Db 181 GAAGCAGTGGAGATACAAATGTGAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 240

QY 316 CTGGAAGTCTTCAAGTCAAGTCTGCTCTTCAAGCCTCTCTGAGGCTGATGGAGGC 375
Db 241 CTGGAAGTCTTCAAGTCAAGTCTGCTCTTCAAGCCTCTCTGAGGCTGATGGAGGC 300

QY 376 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGAACTGGGATGTGTACAAAGTGTATCTAT 435
Db 301 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360

QY 436 TATAAGTGTGAGAGCTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 495
Db 361 TATAAGTGTGAGAGCTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 420

QY 496 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555
Db 421 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480

QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 591
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 516

RESULT 11

US-09-803-715-1
Sequence 1, Application US/0909715
Publication No. US20030003502A1
GENERAL INFORMATION:
APPLICANT: Jaretzky, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Wurzburg, Beth A.
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC
TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A PC REGION OF AN IGE
FILE REFERENCE: AL-8
CURRENT APPLICATION NUMBER: US/09/809,715
CURRENT FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/189,853
PRIOR FILING DATE: 2000-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin ver. 2.1
SEQ ID NO 1
LENGTH: 528
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(528)

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..516
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

Query Match 87.3%; Score 516; DB 9; Length 516;
Best Local Similarity 100.0%; Pred. No. 1.5e-158;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCAGTGAATAGATATTTAAAGGAG 135
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCAGTGAATAGATATTTAAAGGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTTCACCAATGTTTC 195
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAAGTTCACCAATGTTTC 120

QY 196 CACAATGGCAGCCTTTTCAAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 255
Db 121 CACAATGGCAGCCTTTTCAAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 180

QY 256 GAAGCAGTGGAGATACAAATGTGAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 315
Db 181 GAAGCAGTGGAGATACAAATGTGAGAGACAAATTTCAAGTTCAGTTCACCAATGTTTC 240

QY 316 CTGGAAGTCTTCAAGTCAAGTCTGCTCTTCAAGCCTCTCTGAGGCTGATGGAGGC 375
Db 241 CTGGAAGTCTTCAAGTCAAGTCTGCTCTTCAAGCCTCTCTGAGGCTGATGGAGGC 300

QY 376 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGAACTGGGATGTGTACAAAGTGTATCTAT 435
Db 301 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360

QY 436 TATAAGTGTGAGAGCTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 495
Db 361 TATAAGTGTGAGAGCTCTCAAGTCTGATGAGAACCAACATCTCCATTACAAAT 420

QY 496 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555
Db 421 GCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480

QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 591
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 516

RESULT 10

US-10-293-992-3
Sequence 3, Application US/10293992
Publication No. US20040033527A1
GENERAL INFORMATION:
APPLICANT: Jaretzky, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR
TITLE OF INVENTION: CHAIN
FILE REFERENCE: AL-3-C1-1
CURRENT APPLICATION NUMBER: US/10/293,992
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 09/434,193
PRIOR FILING DATE: 1999-11-04
PRIOR APPLICATION NUMBER: 60/107,219
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 516
TYPE: DNA
ORGANISM: Homo sapiens

US-09-809-715-1

Query Match 87.3%; Score 516; DB 10; Length 528;

Best Local Similarity 100.0%; Pred. No. 1.5e-158;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 76 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 135
DB 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAAAATGGTTC 195
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAAAATGGTTC 120

QY 196 CACAATGGCAGCCCTTTCAAGAAGAGACAAATTCAGTCTTGAATATTGTAATGCCAAATTT 255
DB 121 CACAATGGCAGCCCTTTCAAGAAGAGACAAATTCAGTCTTGAATATTGTAATGCCAAATTT 180

QY 256 GAAGCAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315
DB 181 GAAGCAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 316 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCCCTCTGCTGAGGTGGTGGAGGGC 375
DB 241 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCCCTCTGCTGAGGTGGTGGAGGGC 300

QY 376 CAGCCCTCTTCTCAGTGAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 435
DB 301 CAGCCCTCTTCTCAGTGAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360

QY 436 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 495
DB 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420

QY 496 GCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555
DB 421 GCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480

QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

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RESULT 12

US-10-293-992-1

; Sequence 1, Application US/10293992

; Publication No. US20040033527A1

; GENERAL INFORMATION:

; APPLICANT: Jaretsky, Theodore S.

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR

; TITLE OF INVENTION: CHAIN

; FILE REFERENCE: AL-3-C1-1

; CURRENT APPLICATION NUMBER: US/10/293,992

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/434,193

; PRIOR FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/107,219

; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(528)

; OTHER INFORMATION:

US-10-293-992-1

Query Match

87.3%; Score 516; DB 13; Length 528;

Best Local Similarity 100.0%; Pred. No. 1.5e-158;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 76 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 135
DB 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTAAAGGAGAG 60

QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAAAATGGTTC 195
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAAAATGGTTC 120

QY 196 CACAATGGCAGCCCTTTCAAGAAGAGACAAATTCAGTCTTGAATATTGTAATGCCAAATTT 255
DB 121 CACAATGGCAGCCCTTTCAAGAAGAGACAAATTCAGTCTTGAATATTGTAATGCCAAATTT 180

QY 256 GAAGCAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315
DB 181 GAAGCAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 316 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCCCTCTGCTGAGGTGGTGGAGGGC 375
DB 241 CTGGAAGTCTTCAGTGACTGGCTGCTCTCAGGCCCTCTGCTGAGGTGGTGGAGGGC 300

QY 376 CAGCCCTCTTCTCAGTGAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 435
DB 301 CAGCCCTCTTCTCAGTGAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360

QY 436 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 495
DB 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420

QY 496 GCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555
DB 421 GCCACAGTTGAAGCAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480

QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

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RESULT 13

US-09-944-277A-7

; Sequence 7, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect IGE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..699
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

Query Match 87.3%; Score 516; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.8e-158;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 135
Db 1 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60
QY 136 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAAGTTCACCAAAATGGTTC 195
Db 61 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAAGTTCACCAAAATGGTTC 120
QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTCAGTTCACCAAAATGGTTC 255
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTCAGTTCACCAAAATGGTTC 180
QY 256 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 315
Db 181 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
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Db 301 CAGCCCTCTTCTCAGTGGCTGCTTGGAGAACTGGGATGTCAAGGTGATCTAT 360
QY 436 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 495
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
QY 496 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 555
Db 421 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 15
US-10-236-392-29
Sequence 29, Application US/10236392
Publication No. US20040067490A1
GENERAL INFORMATION:
APPLICANT: Anderson, David W
APPLICANT: Boldog, Ferenc L
APPLICANT: Burgess, Catherine, E
APPLICANT: Casman, Stacie J
APPLICANT: Catterton, Elina
APPLICANT: Chapoval, Andrei
APPLICANT: Crabtree, Julie
APPLICANT: Edinger, Shlomit, R
APPLICANT: Ellerman, Karen
APPLICANT: Gerlach, Valerie
APPLICANT: Gorman, Linda
APPLICANT: Grosche, William M
APPLICANT: Gusev, Vladamir

REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..699
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

Query Match 87.3%; Score 516; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.8e-158;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 135
Db 1 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60
QY 136 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAAGTTCACCAAAATGGTTC 195
Db 61 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAAGTTCACCAAAATGGTTC 120
QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTCAGTTCACCAAAATGGTTC 255
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTCAGTTCACCAAAATGGTTC 180
QY 256 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 315
Db 181 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 316 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTCTGAGTGGTGTATGAGAGGC 375
Db 241 CTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTCTGAGTGGTGTATGAGAGGC 300
QY 376 CAGCCCTCTTCTCAGTGGCTGCTTGGAGAACTGGGATGTCAAGGTGATCTAT 435
Db 301 CAGCCCTCTTCTCAGTGGCTGCTTGGAGAACTGGGATGTCAAGGTGATCTAT 360
QY 436 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 495
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
QY 496 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 555
Db 421 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 14
US-09-809-715-3
Sequence 3, Application US/09809715
Publication No. US20030003502A1
GENERAL INFORMATION:
APPLICANT: Jardtzy, Theodore S.
APPLICANT: Garman, Scott Clayton
APPLICANT: Wurzburg, Beth A.
APPLICANT: Kinet, Jean-Pierre
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC
TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
TITLE OF INVENTION: ANTIBODY AND USES THEREOF
FILE REFERENCE: AL-8
CURRENT APPLICATION NUMBER: US/09/809,715

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; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenn
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/559,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 29
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(680)
; US-10-236-392-29

Query Match          58.7%; Score 347; DB 13; Length 757;
Best Local Similarity 80.2%; Pred. No. 7e-103;
Matches 474; Conservative 0; Mismatches 0; Indels 117; Gaps 1;

Qy 1  ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCCTCGTCCA 60
Db 26 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCCTCGTCCA 85
Qy 61  GATGGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGA 120
Db 86  GATGGCGGTGTAGCAGTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCCATGGAATAGA 145
Qy 121 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
Db 146 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 205
Qy 181  TCCACCAAAATGGTTCCCAATGCGCTTTTCCAGAGAGACAAATTCAGTTTGATATT 240
Db 206  TCCACCAAAATGGTTCCCAATGCGCTTTTCCAGAGAGACAAATTCAGTTTGATATT 265
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Qy 241 GTGAATGCCAAATTTGAAGACAGAGTGGAGTAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Qy 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGTCTCTTCAGGCCCTCTCTGTGAG 360
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Qy 361 GTGGTGATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGGTTGAGGAACCTGGGATGTG 420
Db 302 -----TGCCATGGTTGGAGGAACCTGGGATGTG 328
Qy 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATGAGAACCCACAAC 480
Db 329 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATGAGAACCCACAAC 388
Qy 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG 540
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Db 449 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 499
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Job time : 344.307 secs

OM nucleic - nucleic search, using sw model

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		8949.962 Million cell updates/sec

Run on: October 10, 2004, 11:14:29 ; Search time 1994.19 Seconds
(without alignments)

Title: US-10-763-400-10
Perfect score: 591
Sequence: 1 atgqctctgccatgaatc.....acattactgtataaaagct 591

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Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:      27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:  55025578

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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2: em_estnum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
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7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *

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13: gb_esr4: *
14: gb_esr5: *
15: em_estfun: *
16: em_estcom: *
17: em_gss_hum: *

19: em gss pin: *
20: em gss virt: *
21: em gss fun: *
22: em gss nam: *
23: em gss mus: *
24: em gss oxx: *

25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vr: *
28: gb_gss1: *
29: ch_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query [§]		Length	DB	ID	Description
		Match	Match				
1	582.2	98.5	810	12	BG542554	BG542554	60251720
2	567	95.9	834	10	BF679057	BF679057	6021533
3	509.8	86.3	840	12	BG548515	BG548515	6025765
4	470.2	79.6	846	10	BF678252	BF678252	6020851

[illegible]

ALIGNMENTS

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RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5',
mRNA sequence.
BG542554
BG542554.1 GI:13534787
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 810)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1523 row: h column: 14
High quality sequence stop: 667.

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Db 151 ATATTTAAGGAGAGATGTGACTTTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 210
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 QY 361 GTGTGTAGGAGGCCAGCCCTCTCTCTCAGTGCATGCTGGTGGAGGAACCTGGATGTG 420
 Db 391 GTGTGTAGGAGGCCAGCCCTCTCTCTCAGTGCATGCTGGTGGAGGAACCTGGATGTG 450
 QY 421 TACAAGCTGTCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480
 Db 451 TACAAGCTGTCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 510
 QY 481 ATCTCCATTACAAAT--GCCACAGTTGAAGACAGTGGAAACCTAC-TACTGTAGGGGCAAA 537
 Db 511 ATCTCCATTACAAATGGCCACAGTTTGAAGACAGTGGAAACCTACTTACTGTAGGGGCAAA 570
 QY 538 GTGTGGCAGCTGGAC 552
 Db 571 GTGTGGCAGCTGGAC 585

BF678252 846 bp mRNA linear EST 21-DEC-2000
 602086161F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5',
 mRNA sequence.
 BF678252
 BF678252.1 GI:11952147
 EST.
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC http://mgi.nci.nih.gov/
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1071 row: j column: 15
 High quality sequence stop: 609.

FEATURES
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 83"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: Sfil (ggcgctctggcc); Site_2: Sfil
 (ggcattatggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.4

Db 451 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAA- 509
 QY 481 ATCTCCATTACAAATGGCAGTGGAGACAGTGAACCTACTACTGTACGGGCAAGTG 540
 Db 510 ATCTCCATTACAAATGGCAGTGGAGACAGTGAACCTACTACTGTACGGGCAAGTG 569
 QY 541 TGGCAGCTGAGTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
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 BG548515
 BG548515.1 GI:13547180
 EST.
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1544 row: p column: 01
 High quality sequence stop: 590.

FEATURES
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 /clone="IMAGE:4704624"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 77"
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
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 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.9
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 86.3%; Score 509.8; DB 12; Length 840;
 Best Local Similarity 97.3%; Pred. No. 3.3e-140;
 Matches 540; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

QY 1 ATGCTCTCCGATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTTCGCTCCA 60
 Db 31 ATGCTCTCCGATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTTCGCTCCA 90
 QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGTCTCTTGTGAACCTCCATGGAATAGA 120
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 QY 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 180

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 818)
NIH-MGC <http://mgs.nhl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1074 row: n column: 14
High quality sequence stop: 616.

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4251469"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgcctggcc); Site 2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
Kb (range 0.5-4.0 Kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

ORIGIN

Query Match 65.9%; Score 389.4; DB 10; Length 818;
Best Local Similarity 88.9%; Pred. No. 2.3e-104;
Matches 536; Conservative 0; Mismatches 51; Indels 16; Gaps 10;

QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTAGCCCTACTGTCTTCGCTCCA 60
DB 35 ATGGCTCTGCGAAGGAATCCCTACTCTACTGTGTAGCCCTACTGTCTTCGCTCCA 94
QY 61 GATGGCGTGTAGCAGTCCTCTGAAACCTTAAGTCTCTTGAACCTCCATCGAATAGA 120
DB 95 GATGGCGTGTAGCAGTCCTCTGAAACCTTAAGTCTCTTGAACCTCCATCGAATAGA 154
QY 121 ATATTTAAAGGAGAGATGTGACTTACATGTAATGGGAACAATTTCTT-TGAAGTCAG 179
DB 155 ATATTTAAAGGAGAGATGTGACTTACATGTAATGGGAACAATTTCTTGTGAAGTCAG 214
QY 180 TTCCACCAATGGTTCCACAAATGGCAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATA- 238
DB 215 TTCCACCAATGGTTCCACAAATGGCAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAAC 274
QY 239 ---TTTGGAATGCCAAAT--TTGAAGACAGTGGAGAT-ACAAATGTCAGCACCACAAAG 292
DB 275 TACTGGTGAATGCCAAATTTGGAAGACAGTGGGCAATAACAAATGTCAGCACCACAAAG 334
QY 293 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCGCT 352
DB 335 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCGCT 394
QY 353 CTGCTGAGGTGGTGAAGAGGGCCAGCCCTTCCTTCAGGTGCATGGTTGGAGAACT 412
DB 395 CTGCTGAGGTGGTGAAGAGGGCCAGCCCTTCCTTCAGGTGCATGGTTGGAGAACT 454
QY 413 GGGATGCTAC-AAGGTGATCTATTATAAGATGGTGAAGTCTTCAAGTACTGTGTATGAG 471
DB 455 TGGATGTGTACAAAGGTGATCTATTATAGGATGGTGAAGTCTTCAAGTACT-GTATGAG 513

QY 472 AACCAACATCTCCATTACAAATGCCACAGTGTGAAGACAGTGAAC---TACTACTGT 528
DB 514 AACCA-AAAATTTCCATTACAAATGCCACAGTGTGAAGACAGTGAACCTTAACCTTGT 572
QY 529 ACGGGCAAA-GTGGGCGAGCTGGACTA-TGAGTCTGAGCCCTCAACATTACTGTATAAA 586
DB 573 ACGGGCAAAAGTGTGGCAAGTGGACTATTGAGTCTTGAGCCCTCAACATTAGTGTATA 632
QY 587 AAG 589
DB 633 AAG 635

RESULT 7
CF362072 660 bp mRNA linear EST 25-AUG-2003
LOCUS 829457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.
DEFINITION
ACCESSION CF362072
VERSION CF362072.1 GI:34161364
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 660)
Smith,T.P.L., Freking,B.A., Ford,J.J., Valliet,J.L., Fox,J.,
Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.,
A second set of porcine ESTs from a pooled-tissue normalized
library
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.950329.
Plate: SRG8018 row: L column: 4
Seq primer: GTAATACGACTCACTATAGG.

FEATURES
source

Location/Qualifiers
1..660
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3P1G"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."

ORIGIN

Query Match 56.7%; Score 335; DB 14; Length 660;
Best Local Similarity 72.9%; Pred. No. 3.1e-88;
Matches 431; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTAGCCCTACTGTCTTCGCTCCA 60
DB 16 ATGTCTACTCCCATAGGAGTCCCTGCTGTATGATAGTCTGCTCTCTCTCCA 75
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 76 GATGGCATGGCAGCAGTCATCCAGGAATCTCAGGTGTCTTGAATCCCATGGAATAGA 135
QY 121 ATATTTAAAGGAGAGATGTGACTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
DB 136 ATATTTAGAGGAGAGATGTGACTTCTCATCATGTATTTGGGAACGATGCTTGAATATAC 195
QY 181 TCACCAAAATGGTTCCACAAATGGCAGCCCTTTCAGAAAGACACAAATTCAGTTTGAATAT 240

Db 196 CCCACCAATTGGACACACACAAACAACTTTTGAAGTGAAACCTTCAGATTGGGACCTT 255
 QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACGCCAACCAAGTTAATGAG 300
 Db 256 AAGAATGCACAACTTGGGACAGCGGCAATACAGATGCCAAGCAAGACTTTTACAATG 315
 QY 301 AGTGAACCTGTGTACTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 360
 Db 316 AGTGAACCTGTGTACTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 375
 QY 361 GTGGTGATGGAGGGGAGGCGGCTCTTCCTCAGGTGCCATGGTGGAGAACTGGATGTG 420
 Db 376 GTGGTGAGGGAGGCGGCTCTTCCTCTCATGTGTGACGGCTGGAAGATCTGAATGTC 435
 QY 421 TACAAGGTGATCTATTATTAAGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAAC 480
 Db 436 TATAAGGTGATCTACTACAAGGATGGCAAGCGCTCAAGTACTGGTATGAGAACCAAC 495
 QY 481 ATCTCCATTACAAATGCCACAGTTCGAAGACAGTGAAGTCTACTACTGTPACGGGCAAGTG 540
 Db 496 CTCTCCATTACCAATGCCAAGAGAGACAGTGGCTCTTATTGGTGACCGGCTAATT 555
 QY 541 TGGCAGCTGGACTATGAGTGTGAGCGCCCTCAACATTACTGTAAATAAAGCT 591
 Db 556 CAAAAAATACCAAAAACTCTACTACTCTCACCATTACCATACAAACAGAT 606

RESULT 8

BQ573778/c
 LOCUS BQ573778 768 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-H-E20-bav-1-04-0-UI-s1 NCI CGAP Ch1 Homo sapiens cDNA clone
 UI-H-E20-bav-1-04-0-UI 3', mRNA sequence.
 ACCESSION BQ573778
 VERSION BQ573778.1 GI:21477095
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 768)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Prebiterian, Dept. of
 Orthopedics

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 1-41, >AT-rich#Low complexity (matched complement)
 93-129, >LINE2, (matched complement)
 seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

Location/Qualifiers
 1..768
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E20-bav-1-04-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch1"
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
 with a modified polylinker; Site: 1: EcoR I; Site: 2: Not I;
 NCI CGAP Ch1 is a cDNA library containing the following
 tissue(s): Chondrosarcoma Grade II. The library was
 constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adapter, digested with Not I, and cloned directionally
 into pT73-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 TGATCAGCT.
 TAG ISSUE=grade-2-chondrosarcoma
 TAG LIB=UI-H-E20
 TAG_SEQ=ATCTAATATG

ORIGIN

Query Match 49.7%; Score 294; DB 13; Length 768;
 Best Local Similarity 99.7%; Pred. No. 5.6e-76;
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 297 TGAGAGTGAACCTGTGTACTTGAAGTCTTCAAGTGAAGTGGCTCTTCAGGCTCTGC 356
 Db 768 TGAGAGTGAACCTGTGTACTTGAAGTCTTCAAGTGAAGTGGCTCTTCAGGCTCTGC 709
 QY 357 TGAGTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGA 416
 Db 706 TGAGTGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGA 649
 QY 417 TGTGTACAGGTGATCTATTATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCA 476
 Db 648 TGTGTACAGGTGATCTATTATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCA 589
 QY 477 CAACATCTCCATTACAAATGCCACAGTTCACACAGTGGAACTACTACTCTACCGGCA 536
 Db 588 CAACATCTCCATTACAAATGCCACAGTTCACACAGTGGAACTACTACTCTACCGGCA 529
 QY 537 AGTGTGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
 Db 528 AGTGTGGCAGCTGGAGTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 474

RESULT 9

BQ572906 652 bp mRNA linear EST 17-DEC-2002
 DEFINITION BQ572906 RIKEN full-length enriched, adult inner ear Mus musculus
 cDNA clone F930034C11 5', mRNA sequence.
 ACCESSION BQ572906
 VERSION BQ572906.1 GI:27184082
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

LOCUS

BQ572906
 DEFINITION BQ572906 RIKEN full-length enriched, adult inner ear Mus musculus
 cDNA clone F930034C11 5', mRNA sequence.
 ACCESSION BQ572906
 VERSION BQ572906.1 GI:27184082
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 652)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Sult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Sempie, C.A., Secou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, W.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakakawa, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

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Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

Location/Qualifiers

1. .652
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="F930034C11"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"

ORIGIN

Query Match 46.1%; Score 272.6; DB 13; Length 652;
Best Local Similarity 68.6%; Pred. No. 1.2e-69;
Matches 406; Conservative 0; Mismatches 180; Indels 6; Gaps 2;
QY 3 GGCTCTCCCTGGAATCCCTACTCTGTGTGAGCCCTTACTGTCTTCGCTCCAGA 62
DB 29 GCGATGTCTACTGGAAGTCTGCCAGCTGTGCTAGCACTGTCTGTCTGTCTGTA 88
QY 63 TGGCGTGTAGAGTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATGATAGAT 122
DB 89 TGTCTATTGACGCACTGAGAAATCTGTACTGACCTTGGACCCACCATGATAGAT 148

QY 123 ATTTAAAGGAGAGAAATGTGACTTTTACATGTAAATGGGAAACAATTTCTTTGAAGT---CAG 179
DB 149 ATTTACAGGAGAGAAAGTGACCCCTTTCTGTATGGGAAACAATCACCTTCAATGAATC 208
QY 180 TTCCACCBAATGGTTTCCAAATGCGACGCTTTAGAGAGACAAATTCAGATTTGAATAT 239
DB 209 TACTACTAAATGGATCCCAATGTGTACCGTCTCTGAGGTGAACCTCTTCACTTTGGTCA 268
QY 240 TGTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTGAGCAACCAACGAATTAAGA 299
DB 269 TGTGAGTGCCACCGTTCAAGACAGTGGGAAATACATATGTCAGAAACGAAGATGTTTAA 328
QY 300 GAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGCTGCTCTCTCAGGCTCTGCTGA 359
DB 329 GAGTAAACCTGTGTACTTGAATGTAAACCAAGATTGGCTGCTCTCTCAGACATCTGCTGA 388
QY 360 GGTGTGATGAGGCGCCAGCCCTCTCTCCTCAGTGCCATGCTTGGAGGAACCTGGGATGT 419
DB 389 CATGATCTTAGTCCATGATCTCTTGACATCAGATGCCATGGCTGGAGAACTGGAATGT 448
QY 420 GTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGCTGATGAGAACCA 479
DB 449 CCGCAAGGTGATCTACTACAGGAATGACCATGCTTTCAACTACAGTTATGAGAGCC---C 505
QY 480 CATCTCCATTACAATGCCACAGTGGAGACAGTGGACCTTACTTACCGGCAAAAGT 539
DB 506 CGTCTCCATTAGAGAGGCCACACTGAATGACAGTGGACCTTACCCTGNCAGGGCTATCT 565
QY 540 GTGGCAGCTGGACATGATGCTGAGCCCTCAACATCTACTCTAATAAAGCT 591
DB 566 TAGGCAAGTGGAAATGATCTGACAAATTCAGAAATGCTGTAGTAAAGCT 617

RESULT 10
CA448745/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1. .707

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-E10-ayo-p-24-0-UI"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP E10"

/vector="pTV73-Pac (Pharmacia)"

POLYA=yes

Location/Qualifiers

1. .707

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-E10-ayo-p-24-0-UI"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP E10"

/vector="pTV73-Pac (Pharmacia)"

POLYA=yes

Location/Qualifiers

1. .707

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-E10-ayo-p-24-0-UI"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI CGAP E10"

/vector="pTV73-Pac (Pharmacia)"

POLYA=yes

with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP E10 is a cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag located between the Not I site and the (GT)18 tail. The sequence tag for this library is ACACCTGGCAC.

TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-E21
TAG_SEQ=ACACTGGCAC"

ORIGIN

Query Match 39.6%; Score 234; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 3.9e-58;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGGTGGTGTGAGGAGGCGAGCCCTCTTCTCAGTCCCATGGTTGAGGAACCTGGAT 417
|||||
Db 707 GAGGTGGTGTGAGGAGGCGAGCCCTCTTCTCAGTCCCATGGTTGAGGAACCTGGAT 648
|||||

QY 418 GTGTACAAAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTTGATGAGAACAC 477
|||||
Db 647 GTGTACAAAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTTGATGAGAACAC 588
|||||

QY 478 AACATCTCCATTACAAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGGCAAA 537
|||||
Db 587 AACATCTCCATTACAAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGGCAAA 528
|||||

QY 538 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTCTGTAATAAAGCT 591
|||||
Db 527 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAAGTCTGTAATAAAGCT 474
|||||

RESULT 11

CA419024/c
LOCUS CA419024 712 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-E21-bbj-e-19-0-UI s1 NCI CGAP_Ch2 Homo sapiens cDNA clone
UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.
AC419024
VERSION CA419024.1 GI:24781675
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgap@remail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of Orthopedics

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 1-42, >(TAAAA)n#Simple repeat (matched complement)
94-130, >LINE2 (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

Location/Qualifiers
1..712
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="UI-H-E21-bbj-e-19-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ch2"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is TGATCACGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E21
TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 38.7%; Score 228.6; DB 14; Length 712;
Best Local Similarity 97.1%; Pred. No. 1.6e-56;
Matches 231; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 354 TGCTGAGGTGGTGTGAGGAGGCGAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTG 413
|||||
Db 712 TGCTGAGGTGGTGTGAGGAGGCGAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTG 653
|||||

QY 414 GGATGTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 473
|||||
Db 652 GGATGTGTACAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 593
|||||

QY 474 CCACAACATCTCCATTACAAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGG 533
|||||
Db 592 CCACAACATCTCCATTACAAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGG 533
|||||

QY 534 CAAAGTGGCGAGCTGGAGCTATGAGTCTGAGCCCTCAACATTAAGTCTGTAATAAAGCT 591
|||||
Db 532 CAAAGTGGCGAGCTGGAGCTATGAGTCTGAGCCCTCAACATTAAGTCTGTAATAAAGCT 475
|||||

RESULT 12

AW357271
LOCUS AW357271 394 bp mRNA linear EST 25-APR-2001
DEFINITION 40240 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.
AC419024
VERSION AW357271.1 GI:6861277
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 394)

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)

JOURNAL MEDLINE PUBMED COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366

ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
 AW612525
 VERSION
 AW612525.1 GI:7317711
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 669)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
 Seq primer: -40UP from Gibco
 High quality sequence stop: 438.
 Location/Qualifiers
 1..669
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2954053"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI-CGAP Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library.
 (clone)Ds 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldo."

ORIGIN
 Query Match 33.6%; Score 198.8; DB 10; Length 669;
 Best Local Similarity 96.2%; Pred. No. 1.1e-47;
 Matches 203; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 381 CCTTCTCCAGTGGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTATTATAA 440
 Db 669 CCTTCTCCAGTGGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTATTATAA 610
 QY 441 GGATGGTGAAGCTCTCAAGTACTGATGAACCAACATCTCCATTACAAATGCCAC 500
 Db 609 GGATGGTGAAGCTCTCAAGTACTGATGAACCAACATCTCCATTACAAATGCCAC 550
 QY 501 AGTTGAAGACAGTGGAACTTACTACTGTACGGCAAGTGGCAGCTGGACTATGAGTC 560
 Db 549 AGTTGAAGACAGTGGAACTTACTACTGTACGGCAAGTGGCAGCTGGAAATGAGTC 490
 QY 561 TGAGCCCTCAACATTACTGTATAAAGCT 591
 Db 489 TGAGCCCTCAACATTACTGTATAAAGCT 459

RESULT 15
 CB768694
 LOCUS
 DEFINITION
 AW612525:SRP2-00228-E10-A srpb2 (10220) Rattus norvegicus cDNA
 clone srpb2-00228-e10 5', mRNA sequence.
 ACCESSION
 VERSION
 CB768694.1 GI:29857085

KEYWORDS
 SOURCE
 ORGANISM
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 403)
 Angen EST Program.
 Angen Rat EST Program
 Unpublished (2003)
 CONTACT: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00228 row: e column: 10.
 Location/Qualifiers
 1..403
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="srpb2-00228-e10"
 /tissue_type="prostate tissue"
 /clone_lib="srpb2 (10220)"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat
 prostate normalized double selected poly(A+) mRNA size
 fraction > 1 kb"

ORIGIN
 Query Match 29.7%; Score 175.6; DB 14; Length 403;
 Best Local Similarity 69.9%; Pred. No. 6.6e-41;
 Matches 235; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 QY 256 GAAGACAGTGGAGATACAAATGTCTCAGCAACCAAGTAAATGAGTGAACCTGTGTAC 315
 Db 11 GAAGACAGTGGAGATACAAATGTCTCAGCAACCAAGTAAATGAGTGAACCTGTGTAC 70
 QY 316 CTGGAAGTCTTCAGTGAAGTGGTCTCTCTCAGGCTCTGCTGAGGTGGTGTAGAGGC 375
 Db 71 TTGAACNTGATCGANGAGTGGCTGCTGCTCCAAATCTTCTGCTGAGGTGTAGACAAT 130
 QY 376 CAGCCCTTCTCTCAGTGGATGGTGGAGAACTGGATGTGTACAGGTGATCTAT 435
 Db 131 GGATCCTTTGACATCAGATCGGCTAGCTGGAAGAAATGGAAGTCCCAAGGTGATCTAC 190
 QY 436 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACATCTCCATTACAAAT 495
 Db 191 TACAGGACGACATGCTTTCAAGTACTCTTATGACAGCAACACATCTCCATTAGAAAG 250
 QY 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGACTAT 555
 Db 251 GCCACATTTAATGACAGTGGCAGCTTCCACTGTCAGGCTATTTTGAACAGAGTTGAATGT 310
 QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
 Db 311 AAATCTGATAATTCAGTATTGCTGTAGTAAAGAT 346

Search completed: October 10, 2004, 19:44:39
 Job time : 1995.19 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 44.5431 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-11
Perfect score: 1073
Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKVMQLDYSEPLNTIVIKA 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	2 AAR45778	Human dihydrofolate reductase (DHFR)
2	1073	100.0	197	4 AAB31586	Human dihydrofolate reductase (DHFR)
3	1073	100.0	235	2 AAR26064	Human dihydrofolate reductase (DHFR)
4	1073	100.0	257	1 AAP90385	Human dihydrofolate reductase (DHFR)
5	1073	100.0	257	2 AAR05025	Human dihydrofolate reductase (DHFR)
6	1073	100.0	257	2 AAR14772	Human dihydrofolate reductase (DHFR)
7	1073	100.0	257	2 AAR42336	Human dihydrofolate reductase (DHFR)
8	1073	100.0	257	2 AAR24066	Human dihydrofolate reductase (DHFR)
9	1073	100.0	257	2 AAW61190	Human dihydrofolate reductase (DHFR)
10	1073	100.0	257	2 AAW48094	Human dihydrofolate reductase (DHFR)
11	1073	100.0	257	4 AAB74667	Human dihydrofolate reductase (DHFR)
12	1073	100.0	257	4 AAB31584	Human dihydrofolate reductase (DHFR)
13	1073	100.0	257	5 AAB32801	Human dihydrofolate reductase (DHFR)
14	1073	100.0	257	6 ABO01301	Human dihydrofolate reductase (DHFR)
15	1073	100.0	257	7 ADB85536	Human dihydrofolate reductase (DHFR)
16	1073	100.0	257	7 ADD48674	Human dihydrofolate reductase (DHFR)
17	1073	100.0	260	3 AAY96230	Human dihydrofolate reductase (DHFR)
18	1073	100.0	660	4 AAB31593	Human dihydrofolate reductase (DHFR)
19	1073	100.0	756	4 AAB31590	Human dihydrofolate reductase (DHFR)
20	1073	100.0	978	5 AAW48096	Human dihydrofolate reductase (DHFR)
21	1073	100.0	978	5 ASG32803	Human dihydrofolate reductase (DHFR)
22	1032	96.2	193	2 AAR89281	IgE high
23	962.5	99.7	247	2 AAR30483	Human dihydrofolate reductase (DHFR)
24	953	98.8	183	3 AAY96232	Human dihydrofolate reductase (DHFR)
25	951	98.6	182	3 AAY96234	Human dihydrofolate reductase (DHFR)

26	947	88.3	172	2 AAY33185	Human sFC
27	947	88.3	172	3 AAY94211	Human sFC
28	947	88.3	172	4 AAB31587	Human sFC
29	947	88.3	176	3 AAY94210	Human sFC
30	947	88.3	176	4 AAG65597	Amino aci
31	947	88.3	232	4 AAB31585	Amino aci
32	947	88.3	635	4 AAB31594	FC epsilo
33	947	88.3	731	4 AAB31591	Amino aci
34	922	85.9	176	4 AAG65598	Amino aci
35	840.5	78.3	218	6 ABO01302	Human pro
36	775	72.2	281	2 AAR13867	Hybrid FC
37	679	63.3	281	2 AAR13870	FC (gamma)
38	639	59.6	281	2 AAR13872	Recombina
39	617	57.5	201	2 AAY27061	Equine FC
40	617	57.5	255	2 AAR13869	Hybrid FC
41	606	56.5	281	2 AAR13869	Equine hi
42	595	55.5	190	5 AAE18631	Equine FC
43	584	54.4	236	2 AAY27060	Equine FC
44	554	51.6	199	2 AAW81111	Canine FC
45	545	50.8	197	2 AAW81115	Canine FC

ALIGNMENTS

RESULT 1
AAR45778
ID AAR45778 standard; protein; 197 AA.
XX
AC AAR45778;
XX
DT 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX
DE Human dihydrofolate reductase (DHFR).
XX
KW Dihydrofolate reductase; DHFR; marker; transformation.
XX
OS Homo sapiens.
XX
PN WC9403598-Al.
XX
PD 17-FEB-1994.
XX
PF 03-AUG-1993; 93WO-JP001085.
XX
PR 04-AUG-1992; 92JP-0029227.
PR 10-AUG-1992; 92JP-00213002.
PR 08-OCT-1992; 92JP-00270513.
PR 08-OCT-1992; 92JP-00270514.
PR 08-OCT-1992; 92JP-00270515.
XX
(GREC) GREEN CROSS CORP.
PI Ra C, Naito K, Hirama M, Okumura K;
DR WPI; 1994-065687/08.
DR N-PSDB; AAQ55369.
XX
PT Antiallergic peptide derived from high-affinity immunoglobulin E receptor
PT - binds to human immunoglobulin E to block allergic reactions at source.
PS Disclosure; Page 24-25; 37pp; Japanese.
XX
CC The dihydrofolate reductase (DHFR) gene was used in the construction of a
CC vector as a selectable marker. The resulting vector was used to transform
CC DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.3e-77;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 |||||
 Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 |||||

QY 61 STKWFHNGSLSEBTNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQLQSAE 120
 |||||
 Db 61 STKWFHNGSLSEBTNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQLQSAE 120
 |||||

QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 |||||
 Db 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 |||||

QY 181 WOLDYESEPLNITVIKA 197
 |||||
 Db 181 WOLDYESEPLNITVIKA 197
 |||||

RESULT 2
 AAB31586
 ID AAB31586 standard; protein; 197 AA.
 XX
 AC AAB31586;
 DT 30-APR-2001 (first entry)
 XX
 DE A Fc epsilon receptor alpha-chain extracellular domain.
 XX
 KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IGE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IGE syndrome;
 KW internal parasite infection; B cell neoplasia.
 XX
 OS Homo sapiens.
 XX
 PN WO200104310-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-US019070.
 XX
 PR 13-JUL-1999; 99US-0143612P.
 PR 02-MAR-2000; 2000US-0186412P.
 XX
 PA (HESK-) HESKA CORP.
 PA (PROM-) PROMEGA CORP.
 XX
 PI Weber ER, Wood KV, Hall MP;
 XX
 XX WPI; 2001-103082/11.
 DR N-PSDB; AAF24915.
 XX
 PT A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 XX
 PS Claim 16; Page 65; 105pp; English.
 XX
 CC The present sequence represents the extracellular domain of a human Fc
 CC epsilon receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds
 CC to immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a
 CC fusion protein, which also comprises a luminescence inducing protein
 CC domain that induces a substrate to emit light when contacted with the
 CC luminescence inducing protein domain. The fusion protein may be used to
 CC detect IgE. It may also be used to identify a compound capable of
 CC inhibiting Fc epsilonR protein activity. IgE antibody production is
 CC indicative of diseases such as allergies, atopic disease, hyper IGE
 CC syndrome, internal parasite infections and B cell neoplasia. Detection of
 CC IgE production in an animal following therapy is indicative of the
 CC efficacy of the treatment, for example when using treatments intended to
 CC disrupt IgE production
 XX
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 4; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.3e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 |||||
 Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 |||||

QY 61 STKWFHNGSLSEBTNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQLQSAE 120
 |||||
 Db 61 STKWFHNGSLSEBTNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSWLLQLQSAE 120
 |||||

QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 |||||
 Db 121 VMWEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 |||||

QY 181 WOLDYESEPLNITVIKA 197
 |||||
 Db 181 WOLDYESEPLNITVIKA 197
 |||||

RESULT 3
 AAR26064
 ID AAR26064 standard; protein; 235 AA.
 XX
 AC AAR26064;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-FEB-1993 (first entry)
 XX
 XX Human FcERI alpha-subunit and IL-2 hybrid protein.
 DE
 XX High affinity Fc immunoglobulin E receptor; IGE; antibody; interleukin-2;
 KW histamine release; allergy.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Region 26..201
 FT /label= human_FcERI_alpha-subunit
 FT /note= "epitope recognised by new Mab"
 XX
 XX BP499112-A1.
 XX
 PD 19-AUG-1992.
 XX
 XX 03-FEB-1992; 92EP-00101732.
 PF
 XX 11-FEB-1991; 91US-00653936.
 PR
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA
 XX Chizsonite RA, Hakimi J, Kochan JP;
 PI
 XX WPI; 1992-277871/34.
 DR
 XX Monoclonal antibodies bind to alpha sub-unit of Fc IGE receptor - for
 PT treatment and prevention of IGE induced allergic diseases, also for
 PT measuring alpha sub-unit and IGE levels in biological fluids.
 XX
 PS Disclosure; Page 8; 30pp; English.
 XX
 CC This is a preferred protein for use in generating the monoclonal
 CC antibodies of the invention. The protein comprises an epitope of the
 CC human FcERI alpha-subunit to which the cytoplasmic and transmembrane
 CC regions of the IL-2 receptor have been fused. (Cytoplasmic and
 CC transmembrane regions from receptors other IL-2 receptor can be also
 CC used). The specification includes a nucleotide coding sequence which is a
 CC preferred fusion gene (see AAQ27267); the polypeptide which is decoded
 CC from that fusion gene differs from the amino acid sequence AAR26064 as
 CC follows: amino acids 5-7 are Arg-Ile-Leu (not Met-Glu-Ser), amino acid
 CC 209 is Cys (not Lys), amino acid 229 is Ser (not Arg), Arg233 is absent

CC and an additional C-terminal amino acid (Phe) is present. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 235 AA;

Query Match 100.0%; Score 1073; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.2e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120

DB 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120

QY 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

DB 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

QY 181 WOLDYESEPLNITVIKA 197

DB 181 WOLDYESEPLNITVIKA 197

RESULT 4

AAP90385

ID AAP90385 standard; protein; 257 AA.

XX

AC AAP90385;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 01-NOV-1989 (first entry)

XX

XX Alpha subunit of human mast cell IgE surface receptor.

XX

XX Immunoglobulin E receptor alpha subunit; allergies;

XX non-peptide drug design; human.

XX

XX Homo sapiens; (Human); mast cell line.

OS

OS KUB12.

XX

XX WO8905352-A.

XX

PD 15-JUN-1989.

XX

XX 29-NOV-1988; 88WO-US004255.

XX

XX 01-DEC-1987; 87US-00127214.

XX

XX (HARD) HARVARD COLLEGE.

PA (USSH) NAT INST OF HEALTH.

XX

XX Leder P, Benfey P;

XX

XX WPI; 1989-192698/26.

DR N-PSDB; AAN90126.

XX

XX CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.

XX

XX Disclosure; Fig 4; 17pp; English.

XX

XX Immunoglobulin E receptor alpha subunit of human mast cell IgE surface receptor (see corresp. AAN90126). Used to produce antibodies which can diagnose IGE receptor levels measure and treat allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 5.8e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120

DB 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120

QY 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

DB 121 VVMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

QY 181 WOLDYESEPLNITVIKA 197

DB 181 WOLDYESEPLNITVIKA 197

RESULT 5

AAR05025

ID AAR05025 standard; protein; 257 AA.

XX

AC AAR05025;

XX

DT 02-OCT-1990 (first entry)

XX

XX Alpha subunit of human high affinity IgE receptor.

DE

XX high affinity IgE receptor; alpha subunit of IgE receptor; human;

KW allergic response; ss.

XX

XX Synthetic.

XX

XX WO9004640-A.

XX

PD 03-MAY-1990.

XX

XX 18-OCT-1988; 88US-00259065.

XX

XX 18-OCT-1988; 88US-00259065.

XX (USDC) US SEC OF COMMERCE.

XX

XX Kinat JP, Metzger H;

XX

XX WPI; 1990-164023/21.

DR N-PSDB; AAQ04644.

XX

XX DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and derived polypeptides, for therapy and diagnosis of allergies, and studies of IgE receptor interaction.

XX

XX Disclosure; Page ?; -pp; English.

XX

XX The high affinity receptor is a tetrameric complex consisting of 2 gamma subunits and one each of subunits alpha and beta. It is expressed on mast cells and is involved in the allergic response. COS-7 cells cotransfected with cDNA for all 3 intact subunit types (derived from rat basophilic leukaemia cells) express receptor on their surfaces. Detailed study of the receptors is now possible. See also AAQ04643 and AAQ04645-6

XX

SQ Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 5.8e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTITCNGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLIQAASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLIQAASAE 120
 QY 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYESEPLNITVIKA 197
 DB 181 WOLDYESEPLNITVIKA 197

RESULT 6
 AAR14772
 ID AAR14772 standard; protein; 257 AA.
 XX AAR14772;
 AC AAR14772;
 XX 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 03-FEB-1992 (first entry)
 XX Human Fc(epsilon)RI alpha subunit.
 DE Immunoglobulin; receptor; high affinity receptor.
 XX Homo sapiens.
 XX Location/Qualifiers
 FH Key 1..25
 FT Peptide /label= signal
 FT Protein 26..257
 FT /label= alpha_subunit
 FT Domain 80..104
 FT /label= homologous domain
 FT /note= "homologous to residues 163-190"
 FT Domain 163..190
 FT /label= homologous domain
 FT /note= "homologous to residues 80-104"
 FT Region 205..224
 FT /label= transmembrane
 FT Region 225..257
 FT /label= cytoplasmic
 XX USN7626704-N.
 XX PD 15-OCT-1991.
 XX PF 14-DEC-1990; 90US-00626704.
 XX PR 14-DEC-1990; 90US-00626704.
 XX (USSH) NAT INST OF HEALTH.
 XX Kinet JP, Metzger H;
 XX WPI; 1991-346755/47.
 XX N-PSDB; AAQ14736.
 XX DNA coding alpha, beta and gamma-units of ige high affinity receptor -
 PT are used to prepare recombinant polypeptide(s) for treating allergy, drug
 FT screening or monitoring IGE level.
 XX Disclosure; Fig 1; 58pp; English.
 XX A lambda gt11 library was prepared from poly-A RNA isolated from KUB12
 CC cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
 CC cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
 CC and sequenced. This amino acid sequence was deduced from the cDNA clone.
 CC (Note: Revised entry submitted to correct the patent number format of US
 CC Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent

CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX Sequence 257 AA;
 SQ

Query Match 100.0%; Score 1073; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVILTCGNNGFFVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVILTCGNNGFFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLIQAASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLIQAASAE 120
 QY 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYESEPLNITVIKA 197
 DB 181 WOLDYESEPLNITVIKA 197

RESULT 7
 AAR42336
 ID AAR42336 standard; protein; 257 AA.
 XX AAR42336;
 AC AAR42336;
 XX 25-MAR-2003 (revised)
 DT 21-JUN-1994 (first entry)
 XX Human FcεRI alpha.
 DE IGE; immunoglobulin E receptor; beta subunit; basophils; allergy;
 KW aggregation; signal transduction; diagnosis; antagonist.
 XX Homo sapiens.
 OS WO9321317-A1.
 PN 28-OCT-1993.
 PD 16-APR-1993; 93WO-US003419.
 PF 16-APR-1992; 92US-00869933.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX Kinet JP;
 XX WPI; 1993-351727/44.
 XX N-PSDB; AAQ51020.
 XX Immunoglobulin E receptor human beta sub-unit isolation - using 1st
 PT strand reverse transcripts from human basophils as templates for a
 PT polymerase chain reaction, used to treat and diagnose allergic diseases.
 XX Claim 5; Fig 1; 154pp; English.
 XX The sequence is that of the human FcεRI alpha subunit, isolated by using
 CC first strand reverse transcriptase from human basophils by PCR. The gene
 CC and its prod. can be used to identify human beta subunit FcεRI inhibitors
 CC (immunoglobulin E receptor) which inhibit the binding of IGE to its
 CC receptor and inhibit the aggregation function of the receptor or the
 CC signal transducing function related to allergic response. Such inhibitors
 CC can be used for the treatment or prevention of allergic disease. See also
 CC AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 257 AA;
 SQ

Query Match 100.0%; Score 1073; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.8e-77;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKFGENVTLTCGNNFFEVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKFGENVTLTCGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120

QY 121 VMMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180

QY 181 WQDYSESEPLNITVIKA 197
DB 181 WQDYSESEPLNITVIKA 197

RESULT 8
AAW24066
ID AAW24066 standard; protein; 257 AA.

XX AAW24066;
AC
XX
DT 04-FEB-1998 (first entry)

DE Alpha subunit of human high affinity receptor for IgE (human FcERI).
KW alpha subunit; human high affinity receptor; IgE; FcERI; antigen;
KW preformed mediator; histamine; serotonin; leukotriene; IgE level;
KW allergic condition; therapy; allergic response; drug screening;
KW DNA probe; diagnostic assay.
XX Homo sapiens.

PH Key Location/Qualifiers
FT Peptide 1..25
FT /label= signal_peptide
FT Protein 26..257
FT /label= mature_peptide
FT Region 26..204
FT /label= extracellular_portion_of_protein
FT Domain 80..104
FT /label= homologous_domain_1
FT /note= "this region is homologous with amino acids 163-190"
FT Domain 163..190
FT /label= homologous_domain_2
FT /note= "this region is homologous with amino acids 80-104"
FT Region 205..224
FT /label= transmembrane_segment
FT Region 225..257
FT /label= cytoplasmic_domain

XX US5639660-A.
XX
PD 17-JUN-1997.
XX
XX 24-FEB-1988; 88US-00160457.
XX
XX 24-FEB-1988; 88US-00160457.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (HOFF) HOFFMANN LA ROCHE INC.
XX Kochan JP, Kinet JP;
XX
XX WPI; 1997-332052/30.

DR N-PSDB; AAT85615.
XX DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
PT E - used for producing polypeptide(s) which can be used for therapy or to
PT prevent allergic responses or in diagnostic and screening assays.
XX Claim 7; Fig 1A-B; 15pp; English.
PS
CC This sequence represents the alpha subunit of the human high affinity
CC receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC triggers both the release of preformed mediators such as histamine and
CC serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC the release of these mediators that results in an allergic condition. The
CC DNA can be used to produce the human FcERI alpha polypeptides which can
CC be used for therapy or to prevent allergic responses. In drug screening
CC assays or for monitoring IgE levels in patients. The DNA encoding this
CC protein can also be used to produce DNA probes useful in diagnostic
CC assays
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.8e-77;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKFGENVTLTCGNNFFEVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKFGENVTLTCGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120

QY 121 VMMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180

QY 181 WQDYSESEPLNITVIKA 197
DB 181 WQDYSESEPLNITVIKA 197

RESULT 9
AAW61190
ID AAW61190 standard; protein; 257 AA.

XX AAW61190;
AC
XX
DT 07-OCT-1998 (first entry)

DE The alpha chain of a Fc epsilon receptor.
KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW immunoglobulin E; IgE; detection; diagnosis; allergy; atopic disease;
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW flea allergy; heartworm infection.
XX Homo sapiens.
XX
XX WO9823964-A1.
XX
XX 04-JUN-1998.
XX
XX 24-NOV-1997; 97WO-US021651.
XX
XX 26-NOV-1996; 96US-00756387.
XX
XX (HESK-) HESKA CORP.
XX
XX Frank RG, Porter JP, Rushlow KE, Wassom DL;
XX WPI; 1998-322873/28.

DR N-PSDB; AAV36343.
 XX
 XX Detection of non-human immunoglobulin E - by complex formation with human
 PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
 PT disease.
 XX
 XX
 PS Disclosure; Page 37-38; 70pp; English.
 XX
 XX The present sequence represents the alpha chain of the human Fc epsilon
 CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
 CC comprises reacting isolated human Fc epsilon receptor with the test
 CC sample and detecting formation of a IgE-receptor complex. Detection of
 CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
 CC internal parasitic infections or B cell neoplasia, and for measuring
 CC effect of treatments. Most particularly flea allergy in dogs and cats is
 CC detected, and also heartworm infection
 XX
 XX Sequence 257 AA;
 SQ
 Query Match 100.0%; Score 1073; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCGNPFVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCGNPFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLFVSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLFVSDWLLQASAE 120
 QY 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNENHISITNATVEDSGTYCTGKV 180
 DB 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNENHISITNATVEDSGTYCTGKV 180
 QY 181 WLDYSEPLNITVIKA 197
 DB 181 WLDYSEPLNITVIKA 197
 RESULT 10
 ID AAW48094 standard; protein; 257 AA.
 XX
 AC AAW48094;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Human IgE receptor Fc-epsilon-RI alpha chain.
 XX
 KW Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;
 KW fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;
 KW eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /label= Sig_peptide
 FT 26..257
 FT /label= Mat_protein
 FT 26..204
 FT /note= "extracellular domain"
 XX
 PN W0804718-A1.
 XX
 PD 05-FEB-1998.
 XX
 XX 25-JUL-1997; 97WO-EP004066.
 XX
 PR 26-JUL-1996; 96US-00690216.
 XX
 FA (NOVS) NOVARTIS AG.

XX
 PI Digan ME, Lake P, -Gram H;
 XX
 DR WPI; 1998-130705/12.
 DR N-PSDB; AAV20402.
 XX
 PT New fusion polypeptide for, e.g. diagnosing allergies - comprises
 PT immunoglobulin E-binding domain fused to human serum albumin.
 XX
 PS Claim 2; Page 44; 77pp; English.
 XX
 CC This is the amino acid sequence of the dominant form of full-length
 CC native human IgE receptor Fc-epsilon RI alpha chain. A claimed fusion
 CC protein (FP) comprises an IgE binding domain fused to at least one human
 CC serum albumin (HSA) component (see AAW38095), optionally via a peptide
 CC linker, and is especially a dimeric FP (see AAW48096) comprising HSA
 CC fused, at each of its N- and C-termini, to the extracellular domain of Fc
 CC -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP
 CC (see AAV20404); a vector; a process for preparing the FP; a method of
 CC performing gene therapy in humans that comprises removing somatic cells
 CC from a patient, genetically modifying them in culture by insertion of a
 CC polynucleotide that encodes the FP, and reintroducing the modified cells
 CC into the patient so that the FP is expressed by the cells of the patient;
 CC and use of the FP in an in vitro diagnostic assay to determine the level
 CC of IgE or auto-antibodies to Fc epsilon RI in a sample. The products can
 CC be used in the prevention and/or treatment of IgE-mediated allergic
 CC diseases and related disorders such as atopic dermatitis, atopic asthma,
 CC chronic urticaria, hayfever and eczema. Compared with using IgE binding
 CC domain alone, the FP has a longer serum life, and thus greater activity,
 CC without a loss of ability to bind serum IgE or circulating auto-
 CC antibodies
 XX
 SQ Sequence 257 AA;
 Query Match 100.0%; Score 1073; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCGNPFVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCGNPFVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLFVSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLFVSDWLLQASAE 120
 QY 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNENHISITNATVEDSGTYCTGKV 180
 DB 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNENHISITNATVEDSGTYCTGKV 180
 QY 181 WLDYSEPLNITVIKA 197
 DB 181 WLDYSEPLNITVIKA 197
 RESULT 11
 ID AAB74667 standard; protein; 257 AA.
 XX
 AC AAB74667;
 XX
 DT 19-JUN-2001 (first entry)
 XX
 DE Human immunoglobulin E receptor I alpha subunit protein.
 XX
 KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
 KW immunoassay; detection.
 XX
 OS Homo sapiens.
 XX
 PN W0200111010-A2.
 XX

PD 15-FEB-2001.
 XX 02-AUG-2000; 2000WO-US021097.
 PF 09-AUG-1999; 99US-0147860P.
 XX (GENA-) GENAISSANCE PHARM INC.
 PA Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
 PI Stephens JC;
 PI WPI; 2001-202766/20.
 DR N-PSDB; AAF97964.
 XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms
 PT in the immunoglobulin E receptor I alpha subunit gene.
 PT Claim 10; Fig 3; 99pp; English.
 XX The present invention describes an isolated polynucleotide (I) comprising
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
 CC gene or its fragment. The polymorphic variant comprises at least one
 CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
 CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
 CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
 CC a position corresponding to nucleotide 530. (I) can be used in gene
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
 CC encoded by (I) is useful in drug screening assays and in assays to
 CC measure the binding affinity of one or more candidate drugs targeting
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
 CC solution and also reacts with (II) on Western or immunoblots of
 CC polyacrylamide gels on membrane supports or substrates. (III) is also
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
 CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
 CC to AAF98140 represent IGERA gene polymorphism detection primers; and
 CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
 CC the amplification of the present invention. The present sequence
 CC represents the human IGERA protein used in the present invention
 CC
 XX Sequence 257 AA;
 SQ
 Query Match 100.0%; Score 1073; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQOVNESEPVYLEVFSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQOVNESEPVYLEVFSDWLLQASAE 120
 QY 121 VVMGQPLFLRCHGRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 DB 121 VVMGQPLFLRCHGRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 QY 181 WQDYSEPLNITVIKA 197
 DB 181 WQDYSEPLNITVIKA 197
 RESULT 12
 AAB31584
 ID AAB31584 standard; protein; 257 AA.
 XX AAB31584;
 AC
 XX 30-APR-2001 (first entry)
 DT
 XX

DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.
 XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;
 KW luminescence inducing protein; allergy; hyper IgE syndrome;
 KW internal parasite infection; B cell neoplasia.
 XX Homo sapiens.
 OS
 XX WO200104310-A1.
 PN 18-JAN-2001.
 XX 13-JUL-2000; 2000WO-US019070.
 PF 13-JUL-1999; 99US-0143612P.
 PR 02-MAR-2000; 2000US-0166412P.
 XX (HESK-) HESKA CORP.
 PA (PROM-) PROMEGA CORP.
 PI Weber ER, Wood KV, Hall MP;
 PI WPI; 2001-103082/11.
 DR N-PSDB; AAF24911.
 XX A fusion protein, comprising an Fc epsilon receptor domain and a
 PT luminescence inducing protein domain that induces a LP substrate to emit
 PT light when contacted with the LP domain, useful for detecting
 PT immunoglobulin (Ig) E.
 PT Claim 16; Page 60; 105pp; English.
 XX The present sequence represents a human Fc epsilon receptor (Fc epsilonR)
 CC alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilonR
 CC domain is used to produce a fusion protein, which also comprises a
 CC luminescence inducing protein domain that induces a substrate to emit
 CC light when contacted with the luminescence inducing protein domain. The
 CC fusion protein may be used to detect IgE. It may also be used to identify
 CC a compound capable of inhibiting Fc epsilonR protein activity. IgE
 CC antibody production is indicative of diseases such as allergies, atopic
 CC disease, hyper IgE syndrome, internal parasite infections and B cell
 CC neoplasia. Detection of IgE production in an animal following therapy is
 CC indicative of the efficacy of the treatment, for example when using
 CC treatments intended to disrupt IgE production
 XX Sequence 257 AA;
 SQ
 Query Match 100.0%; Score 1073; DB 4; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQOVNESEPVYLEVFSDWLLQASAE 120
 DB 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQOVNESEPVYLEVFSDWLLQASAE 120
 QY 121 VVMGQPLFLRCHGRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 DB 121 VVMGQPLFLRCHGRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 QY 181 WQDYSEPLNITVIKA 197
 DB 181 WQDYSEPLNITVIKA 197
 RESULT 13
 ABG32801
 ID ABG32801 standard; protein; 257 AA.
 XX ABG32801;
 AC

XX 29-NOV-2002 (first entry)
 XX Human IgE receptor FcpepsilonRIalpha.
 XX Human; IgE; receptor; FcpepsilonRIalpha; HSA; human serum albumin;
 KW anti-allergic; dermatological; anti-inflammatory; antiasthmatic;
 KW IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;
 KW atopic dermatitis; atopic asthma; chronic urticaria.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..25
 FT Protein /label= Signal_peptide
 FT Region /label= Mature_FcpepsilonRIalpha
 FT /label= IGE_binding_domain
 FT /note= "This region is specifically claimed in claim 5"
 XX US6423512-B1.
 XX 23-JUL-2002.
 XX 21-JUL-1997; 97US-00897956.
 XX 26-JUL-1996; 96US-0022689P.
 XX (NOVS) NOVARTIS AG.
 XX Digan ME, Lake P, Gram H;
 DR WPI; 2002-672940/72.
 DR N-PSDB; ABS52959.
 XX New fusion IgE-binding polypeptide, useful for the prevention and
 PT treatment of systemic allergy and/or other IgE-receptor-mediated
 PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.
 XX Claim 5; Fig 13; 49pp; English.
 XX The invention relates to a new fusion polypeptide or its pharmaceutically
 CC acceptable salt comprises at least one IgE-binding domain fused to at
 CC least one human serum albumin (HSA) component, where the IgE-binding
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell
 CC transformed with the polynucleotide; (4) a method of preparing the fusion
 CC protein comprising transforming a host cell with a vector comprising a
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion
 CC polypeptide in the cell, and recovering the fusion polypeptide from the
 CC host cell, optionally in the form of its salt; and (5) a vector for
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of
 CC formula (I), (II), (III), (IV), or (V) or its salts (R₁-L-R₂ (I), R₂-
 CC L-R₁ (II), R₁-L-R₂-L-R₁ (III), R₁-L-R₁-L-R₂ (IV), R₂-L-R₁-L-R₁-
 CC L-R₂ (V), where R₁ = the polypeptide (a) or its truncation at the carboxy
 CC terminus by 1-12 amino acids and R₂ = a polypeptide selected from the
 CC sequence defined by residues Asp25-Leu609 the human HSA sequence
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
 CC amino acids and L = independently a chemical bond, where the vector is
 CC PXMT3-Rla-HAS-Rla). The compositions and methods of the present invention
 CC are useful for the prevention and treatment of systemic allergy and other
 CC IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma
 CC and chronic urticaria. The IgE-binding polypeptide have a more prolonged
 CC effective serum life. The IgE-binding polypeptide have a more prolonged
 CC effective clinical utility in the treatment of
 CC allergy, as well as improved activity in a more efficient and cost-
 CC effective manner. The present sequence is the human IgE receptor
 CC FcpepsilonRIalpha used to make the fusion protein of the invention
 XX Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 5; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFFAPDGVLAPOKPKVSLNPPWNRIFKGENVTLTCGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFFAPDGVLAPOKPKVSLNPPWNRIFKGENVTLTCGNFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 QY 121 VVMGQPLFLRCHGRNWDVYKVIYKDGALKYWYENHNISITNATVEDSGTYCTGKV 180
 DB 121 VVMGQPLFLRCHGRNWDVYKVIYKDGALKYWYENHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKA 197
 DB 181 WOLDYSEPLNITVIKA 197
 RESULT 14
 ABO01301
 ID ABO01301_standard; protein; 257 AA.
 XX ABO01301;
 AC ABO01301;
 XX 07-AUG-2003 (first entry)
 DT Human protein NOV8a.
 XX DE
 XX KW Human; NOV8; cardiomyopathy; atherosclerosis; hypertension;
 KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
 KW neoplasm; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
 KW cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2003023008-A2.
 XX PD 20-MAR-2003.
 XX PF 09-SEP-2002; 2002WO-US028596.
 XX PR 07-SEP-2001; 2001US-0318120P.
 PR 10-SEP-2001; 2001US-0318130P.
 PR 12-SEP-2001; 2001US-0318430P.
 PR 17-SEP-2001; 2001US-0318765P.
 PR 17-SEP-2001; 2001US-0322781P.
 PR 19-SEP-2001; 2001US-0322816P.
 PR 20-SEP-2001; 2001US-0323519P.
 PR 20-SEP-2001; 2001US-0323631P.
 PR 25-SEP-2001; 2001US-0323636P.
 PR 25-SEP-2001; 2001US-0324989P.
 PR 26-SEP-2001; 2001US-0325091P.
 PR 15-FEB-2002; 2002US-0357303P.
 PR 28-FEB-2002; 2002US-0360973P.
 PR 28-MAR-2002; 2002US-0366131P.
 PR 25-MAR-2002; 2002US-0367753P.
 PR 02-APR-2002; 2002US-0369479P.
 PR 10-MAY-2002; 2002US-0379532P.
 PR 17-MAY-2002; 2002US-0381664P.
 PR 17-MAY-2002; 2002US-0381672P.
 PR 28-MAY-2002; 2002US-0383651P.
 PR 28-MAY-2002; 2002US-0384012P.
 PR 19-JUN-2002; 2002US-0390155P.
 PR 06-SEP-2002; 2002US-00390155.
 XX

(CURA-) CURAGEN CORP.

Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
 Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
 Patterson M, Pena CE, Tchernev VT, Padigaru M, Gusev VI;
 Malyankar UV, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
 Grosse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
 Larocheville WJ, Shimkets RA, Crabtree J, Rastelli L, Voss EZ;
 Boldog FI, Edinger SR, Millet I, Macdougall JR, Ellerman K;
 Chapoval A;

WPI; 2003-313246/30.
 N-PSDB; ACD06182.

New polypeptides and polynucleotides having properties related to stimulation of biochemical or physiological responses in a cell or tissue, useful for diagnosing or preventing e.g. atherosclerosis, hypertension, prostate cancer.

Claim 2; Page 133; 849pp; English.

The invention relates to an isolated polypeptide comprising one of 127 sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature form of NOVX, an amino acid sequence comprising which is at least 95% identical to NOVX or an amino acid sequence comprising one or more conservative substitutions in NOVX. Also included are nucleic acids encoding NOVX proteins, determining the presence or amount of NOVX or NOVX DNA in a sample (by introducing the sample to an antibody that binds immunospecifically to the polypeptide, and determining the presence or amount of antibody bound to the polypeptide), determining the presence or or predisposition to a disease associated with altered levels of expression of NOVX or NOVX DNA in a first mammalian subject, identifying an agent that binds to NOVX, identifying a potential therapeutic agent for treatment of a pathology related to aberrant expression or aberrant physiological interactions of NOVX, screening for a modulator of activity of or of latency or predisposition to a pathology associated with NOVX, a vector comprising NOVX DNA, a cell comprising the vector (used to produce NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides are useful as a marker for cell or tissue type, and in diagnosing and treating pathologies, diseases, conditions or disorders associated with NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, prostate cancer, diabetes, metabolic disorders, neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious diseases, anorexia, cancer-associated cachexia, neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's disease), immune disorders, haematopoietic disorders, dyslipidaemias, and wasting disorders associated with chronic diseases. These may also be used to screen for molecules which inhibit or enhance NOVX activity or function, and for detecting specific cell types. These may also be used in chromosome mapping, gene therapy, tissue typing, and in forensic biology. The present sequence represents a NOVX protein

Query Match 100.0%; Score 1073; DB 6; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPAMESPTLLCVALLFPADGVLAQPKPKVSLNPPNRRIFKGENVTLTCGNPNFEVS 60
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 61 STKWFHNGSLSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLEVFSDDLQASAE 120

121 VMMEGQPLFLCHGWRNDVVKVIYKDGKALKWYENHNISITNATVDSGTGYCTGKV 180
 121 VMMEGQPLFLCHGWRNDVVKVIYKDGKALKWYENHNISITNATVDSGTGYCTGKV 180

181 WOLDYSEPLNITVKA 197

Db 181 WOLDYSEPLNITVKA 197

RESULT 15
 ADB85536
 ID ADB85536 standard; protein; 257 AA.
 XX
 AC ADB85536;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human immunoglobulin E high affinity receptor alpha subunit protein.
 XX
 KW alpha subunit; high affinity receptor for immunoglobulin E; FCERI;
 KW mast cell; basophil; histamine; serotonin; allergic condition;
 KW anti-allergic; allergic response; drug screening assay; immunoglobulin E;
 KW human.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Misc-difference 221 Location/Qualifiers
 FT /note= "Encoded by OGA"
 FT Misc-difference 253
 FT /note= "Encoded by AAC"
 XX
 PN US6602983-B1.
 XX
 PD 05-AUG-2003.
 XX
 PF 22-SEP-1994; 94US-00310902.
 XX
 PR 24-FEB-1988; 88US-00160457.
 PR 30-OCT-1991; 91US-00785127.
 PR 29-MAY-1993; 93US-00066640.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kinet JP, Kochan JP;
 DR WPI; 2003-669612/63.
 DR N-PSDB; ADB85535.
 XX
 PT New alpha subunit of the human high affinity receptor for immunoglobulin E polypeptides, useful as antagonists to prevent allergic response, as reagents in drug screening assays, or for monitoring immunoglobulin E levels in patients.
 XX
 PS Claim 1; Fig 1; 9pp; English.
 XX
 CC This invention relates to a novel purified polypeptide corresponding to the alpha subunit of the human high affinity receptor for immunoglobulin E (FcERI) and the DNA sequence which encodes it. The receptor of the invention is found exclusively on mast cells, basophils and related cells. Activation of the receptor triggers the release of preformed mediators such as histamine and serotonin which may result in allergic conditions. Compounds which modulate FcERI activity may have anti-allergic activity. The polypeptide of the invention may be useful as an antagonist for preventing allergic response, as a reagent in drug screening assays, as a therapeutic or for monitoring immunoglobulin E levels in patients. The DNA sequences may be useful for producing the polypeptide or for synthesising cDNA sequences to construct DNA probes used in diagnostic assays. The present sequence is the amino acid sequence of the alpha subunit of the human FcERI receptor of the invention.

Query Match 100.0%; Score 1073; DB 7; Length 257;
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAPAMESPTLLCVALLFPADGVLAQPKPKVSLNPPNRRIFKGENVTLTCGNPNFEVS 60

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Db      1  MAPAMESPTLLCVALLFFAPDGVLA VPOKPKVSLNPPWNRIFKGENVTLCNGNPFVS 60
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Db      61  STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
        |||||
QY      121  VMMEQOPLFLRCHGWRNDVYKVIYKDGEBALKYWIENHNISITNATVEDSGTYCTGKV 180
        |||||
Db      121  VMMEQOPLFLRCHGWRNDVYKVIYKDGEBALKYWIENHNISITNATVEDSGTYCTGKV 180
        |||||
QY      181  WOLDYESEPLNITVIKA 197
        |||||
Db      181  WOLDYESEPLNITVIKA 197
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Search completed: October 6, 2004, 09:03:07
 Job time : 45.5431 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 12.8578 Seconds
(without alignments)
790.984 Million cell updates/sec

Title: US-10-763-400-11
Perfect score: 1073
Sequence: 1 MAPAMESPTLLCVALLFFAP.....GKWWQDYSEPLNITVIKA 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	100.0	197	2	US-08-756-387B-11
2	1073	100.0	197	4	US-09-285-873-11
3	1073	100.0	197	4	US-09-944-277A-11
4	1073	100.0	257	1	US-07-869-933-11
5	1073	100.0	257	2	US-08-756-387B-2
6	1073	100.0	257	3	US-09-103-663-11
7	1073	100.0	257	4	US-09-285-873-2
8	1073	100.0	257	4	US-08-897-956A-1
9	1073	100.0	257	4	US-09-944-277A-2
10	1073	100.0	978	4	US-08-897-956A-3
11	1067	99.4	197	3	US-08-788-954-2
12	1032	96.2	193	2	US-08-756-387B-1
13	1032	96.2	193	5	PT-US95-08401-1
14	947	88.3	172	4	US-08-756-387B-13
15	947	88.3	172	4	US-09-285-873-13
16	947	88.3	172	4	US-08-245-764-9
17	947	88.3	172	4	US-09-944-277A-13
18	947	88.3	232	1	US-07-869-933-13
19	947	88.3	232	2	US-08-756-387B-6
20	947	88.3	232	3	US-08-103-663-13
21	947	88.3	232	4	US-09-285-873-6
22	947	88.3	232	4	US-09-944-277A-6
23	617	57.5	201	3	US-09-015-734-12
24	617	57.5	201	4	US-09-515-311-12
25	617	57.5	255	3	US-09-015-734-2
26	617	57.5	255	4	US-09-515-311-2
27	584	54.4	236	3	US-09-015-734-7

28	584	54.4	236	4	US-09-515-311-7	Sequence 7, Appli
29	554	51.6	199	3	US-08-833-488B-14	Sequence 14, Appl
30	545	50.8	197	3	US-08-833-488B-4	Sequence 4, Appli
31	545	50.8	197	3	US-08-833-488B-28	Sequence 28, Appl
32	545	50.8	253	3	US-08-833-488B-20	Sequence 20, Appl
33	543	50.6	197	3	US-08-833-488B-9	Sequence 9, Appli
34	538	50.1	431	4	US-09-592-998C-9	Sequence 9, Appli
35	538	50.1	435	4	US-09-592-998C-10	Sequence 10, Appl
36	522.5	48.7	199	2	US-08-768-964-12	Sequence 12, Appl
37	522.5	48.7	199	3	US-09-005-299-12	Sequence 12, Appl
38	522.5	48.7	199	3	US-09-515-431-12	Sequence 12, Appl
39	522.5	48.7	263	2	US-08-768-964-2	Sequence 2, Appli
40	522.5	48.7	263	3	US-09-005-299-2	Sequence 2, Appli
41	522.5	48.7	263	3	US-09-515-431-2	Sequence 2, Appli
42	516	48.1	173	3	US-08-833-488B-31	Sequence 31, Appl
43	516	48.1	229	3	US-08-833-488B-24	Sequence 24, Appl
44	491	45.8	174	2	US-08-768-964-13	Sequence 13, Appl
45	491	45.8	174	3	US-09-005-299-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-756-387B-11
; Sequence 11, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-11

Query Match 100.0%; Score 1073; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIKGENVTITCNGNFFEVS 60
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QY 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WOLDYSEPLNITVIKA 197
DB 181 WOLDYSEPLNITVIKA 197

RESULT 2

US-09-285-873-11
; Sequence 11, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-11

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Best Local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120
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DB 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
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DB 181 WOLDYSEPLNITVIKA 197

RESULT 3

US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match 100.0%; Score 1073; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.7e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPAMESPTLLCVALLFPADGVLPQPKVSLNPPWNRIFKGNVTLTCGNFFEVS 60
DB 1 MAPAMESPTLLCVALLFPADGVLPQPKVSLNPPWNRIFKGNVTLTCGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120
QY 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WOLDYSEPLNITVIKA 197

Db 181 WOLDYSEPLNITVIKA 197

RESULT 4

US-07-869-933-11

Sequence 11, Application US/07869933

Patent No. 5770396

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933

FILING DATE: 19920416

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/154 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-869-933-11

Query Match 100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 3.9e-98;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNPFVS 60

Db 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNPFVS 60

QY 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

Db 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

QY 121 VMMEGQPLFLRCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYICTGV 180

Db 121 VMMEGQPLFLRCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYICTGV 180

QY 181 WOLDYSEPLNITVIKA 197

Db 181 WOLDYSEPLNITVIKA 197

RESULT 5

US-08-756-387B-2

Sequence 2, Application US/08756387B

Patent No. 5945294

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wassom, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

ADDRESSEE: Heska Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,387B

FILING DATE: No. 5945294ember 26, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-756-387B-2

Query Match 100.0%; Score 1073; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 3.9e-98;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNPFVS 60

Db 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCGNPFVS 60

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QY 121 VMMEGQPLFLRCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYICTGV 180

Db 121 VMMEGQPLFLRCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYICTGV 180

QY 181 WOLDYSEPLNITVIKA 197

Db 181 WOLDYSEPLNITVIKA 197

RESULT 6

US-09-103-663-11

Sequence 11, Application US/09103663D

Patent No. 6171803

GENERAL INFORMATION:

APPLICANT: Kinet et al.

TITLE OF INVENTION: Isolation, characterization, and use of the human beta

TITLE OF INVENTION: subunit of the high affinity receptor for

TITLE OF INVENTION: immunoglobulin E.

FILE REFERENCE: 50490

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT FILING DATE: 1998-06-23

EARLIER APPLICATION NUMBER: 07/869,933

EARLIER FILING DATE: 1992-04-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

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/ SEQ ID NO 11
/ LENGTH: 257
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-103-663-11

Query Match      100.0%; Score 1073; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 7
US-09-285-873-2
/ Sequence 2, Application US/09285873
/ Patent No. 6309832
/ GENERAL INFORMATION:
/ APPLICANT: Frank, Glenn R.
/ APPLICANT: Porter, James P.
/ APPLICANT: Rushlow, Keith E.
/ APPLICANT: Wasson, Donald L.
/ TITLE OF INVENTION: Method to Detect IgE
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carol Talkington Verser, Ph.D.
/ ADDRESSEE: Heskia Corporation
/ STREET: 1825 Sharp Point Drive
/ CITY: Fort Collins
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80525
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: WordPerfect for Windows, Version 7.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/285,873
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/756,387
/ FILING DATE: No. 6309832ember 26, 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Verser, Carol Talkington
/ REGISTRATION NUMBER: 37,459
/ REFERENCE/DOCKET NUMBER: DI-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 970/493-7272
/ TELEFAX: 970/484-9505
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-285-873-2

Query Match      100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 8
US-08-897-956A-1
/ Sequence 1, Application US/08897956A
/ Patent No. 6423512
/ GENERAL INFORMATION:
/ APPLICANT: Mary Ellen Digan
/ APPLICANT: Philip Lake
/ APPLICANT: Hermann Gram
/ TITLE OF INVENTION: Fusion Polypeptides
/ FILE REFERENCE: 600-7244/CPA
/ CURRENT APPLICATION NUMBER: US/08/897,956A
/ PRIOR FILING DATE: 1997-07-21
/ PRIOR APPLICATION NUMBER: 60/022,689
/ PRIOR FILING DATE: 1996-07-26
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 257
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-08-897-956A-1

Query Match      100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNDVKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 9
US-09-944-277A-2
/ Sequence 2, Application US/09944277A
/ Patent No. 6682894
/ GENERAL INFORMATION:
/ APPLICANT: Frank, Glenn R.
/ APPLICANT: Porter, James P.
/ APPLICANT: Rushlow, Keith E.
/ APPLICANT: Wasson, Donald L.
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Tue Oct 12 09:19:21 2004

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; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match 100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLQSAE 120
Db 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLQSAE 120
QY 121 VMMEGQPLFLRCHGWRWDVYKVIYKDGALKYWNHNHISITNATVEDSGTYCTGKV 180
Db 121 VMMEGQPLFLRCHGWRWDVYKVIYKDGALKYWNHNHISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 10
US-08-897-956A-3
; Sequence 3, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26

; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-08-897-956A-3

Query Match 100.0%; Score 1073; DB 4; Length 978;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLQSAE 120
Db 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLQSAE 120
QY 121 VMMEGQPLFLRCHGWRWDVYKVIYKDGALKYWNHNHISITNATVEDSGTYCTGKV 180
Db 121 VMMEGQPLFLRCHGWRWDVYKVIYKDGALKYWNHNHISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 11
US-08-788-954-2
; Sequence 2, Application US/08788954
; Patent No. 6090384
; GENERAL INFORMATION:
; APPLICANT: RA, CHISEI
; APPLICANT: NAITO, KOJI
; APPLICANT: HIRAWA, MINORU
; APPLICANT: OKUMURA, KO
; TITLE OF INVENTION: ANTIALLERGIC COMPOSITION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SUGHRUB, MION, ZINN, MACPEAK, & SEAS
; STREET: 2100 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,954
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US/08/474,188
; FILING DATE:
; APPLICATION NUMBER: US 08/023,912
; FILING DATE: 26-FEB-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-788-954-2

Query Match 99.4%; Score 1067; DB 3; Length 197;

Best Local Similarity 99.5%; Pred. No. 1.1e-97;

Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 DB 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVS 60
 QY 61 STKWFHNGSLSEETSSNINIVAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 DB 61 STKWFHNGSLSEETSSNINIVAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKA 197
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 12

US-08-765-536-1

; Sequence 1, Application US/08765536

; Patent No. 5962634

; GENERAL INFORMATION:

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Sutton, Brian J.

; APPLICANT: McDonnell, James M.

; APPLICANT: Gould, Hannah J.

; APPLICANT: Korngold, Robert

; APPLICANT: Beavil, Andrew J.

; TITLE OF INVENTION: Ige Antagonists

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5962634ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,536

; FILING DATE: April 30, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,943

; FILING DATE: 08-JUL-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1619

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-765-536-1

Query Match

Best Local Similarity 96.2%; Score 1032; DB 2; Length 193;

Pred. No. 3e-94;

Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVSSTKWF 65
 DB 1 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVSSTKWF 60
 QY 66 HNGSLSEETSSNINIVAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAEVWMEG 125
 DB 61 HNGSLSEETSSNINIVAKFEDSGEYKCOHQVNESEPVYLEVFSWLLLOASAEVWMEG 120
 QY 126 QPLFLRCHGWRNDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKVWQLDY 185
 DB 121 QPLFLRCHGWRNDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKVWQLDY 180
 QY 186 ESEPLNITVIKA 197
 DB 181 ESEPLNITVIKA 192

RESULT 13

PCT-US95-08401-1

; Sequence 1, Application PC/TUS9508401

; GENERAL INFORMATION:

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Sutton, Brian J.

; APPLICANT: McDonnell, James M.

; APPLICANT: Gould, Hannah J.

; APPLICANT: Korngold, Robert

; APPLICANT: Beavil, Andrew J.

; TITLE OF INVENTION: Ige Antagonists

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08401

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,943

; FILING DATE: 08-JUL-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TJU-1597

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-08401-1

Query Match

Best Local Similarity 96.2%; Score 1032; DB 5; Length 193;

Pred. No. 3e-94;

Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLTCNGNFFEVSSTKWF 65
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Db 1 EPTLLCVALLFPAPGVLAQPKVSLNPPWNRIFKGNVTLCNGNPFVSTKWF 60
QY 66 HNGSLSEETNSSLNIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEG 125
Db 61 HNGSLSEETNSSLNIVNAKFDSEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEG 120
QY 126 QPLFLCHGWRNWDVYKVIYKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDY 185
Db 121 QPLFLCHGWRNWDVYKVIYKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDY 180
QY 186 ESEPLNITVIKA 197
Db 181 ESEPLNITVIKA 192

RESULT 14
US-08-756-387B-13
; Sequence 13, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Haska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/494-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 88.3%; Score 947; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.3e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 VPQPKVSLNPPWNRIFKGNVTLCNGNPFVSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPWNRIFKGNVTLCNGNPFVSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNWDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNWDVYKVIY 120
QY 146 YKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197
Db 121 YKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

Search completed: October 6, 2004, 09:04:38
Job time : 13.8578 secs

RESULT 15
US-09-285-873-13
; Sequence 13, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Haska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-13

Query Match 88.3%; Score 947; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.3e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 VPQPKVSLNPPWNRIFKGNVTLCNGNPFVSTKWFHNGSLSEETNSSLNIVNAKF 85
Db 1 VPQPKVSLNPPWNRIFKGNVTLCNGNPFVSTKWFHNGSLSEETNSSLNIVNAKF 60
QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNWDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNWDVYKVIY 120
QY 146 YKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197
Db 121 YKDGKALKYWHNNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

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Sequence 180, Appli
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Sequence 69, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 93, Appli
Sequence 68, Appli

ALIGNMENTS

ALIGNMENTS

US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/464-9505

RESULT 1

US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/464-9505

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	9	US-09-944-277A-11
2	1073	100.0	257	9	US-09-944-277A-2
3	1073	100.0	257	12	US-10-236-392-28
4	1073	100.0	257	14	US-10-384-850-45
5	947	88.3	172	9	US-09-944-277A-13
6	947	88.3	172	9	US-09-245-764-9
7	947	88.3	172	12	US-10-293-992-4
8	947	88.3	172	12	US-10-687-109-9
9	947	88.3	176	10	US-09-809-715-2
10	947	88.3	176	12	US-10-293-992-2
11	947	88.3	232	9	US-09-944-277A-6
12	922	85.9	176	10	US-08-809-715-4
13	840.5	78.3	218	12	US-10-236-392-30
14	617	57.5	201	15	US-10-434-817-12
15	617	57.5	255	15	US-10-434-817-2

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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 60.1562 Seconds
(without alignments)
1053.831 Million cell updates/sec

Title: US-10-763-400-11
Perfect score: 1073
Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKVMQDYSEPLNITVIKA 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
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- 18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match          100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTGNNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAE 120
QY 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WQDYSEPLNITVIKA 197
Db 181 WQDYSEPLNITVIKA 197

RESULT 2
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Forster, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,453
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match          100.0%; Score 1073; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTGNNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLTGNNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAE 120
QY 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGRWMDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WQDYSEPLNITVIKA 197
Db 181 WQDYSEPLNITVIKA 197

RESULT 3
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, Li, Li
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Smithson, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
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PRIOR FILING DATE: 2002-02-15
 PRIOR APPLICATION NUMBER: US60/367,753
 PRIOR FILING DATE: 2002-03-25
 PRIOR APPLICATION NUMBER: US60/369,479
 PRIOR FILING DATE: 2002-04-02
 PRIOR APPLICATION NUMBER: US09/659,634
 PRIOR FILING DATE: 2000-09-12
 PRIOR APPLICATION NUMBER: US60/318,120
 PRIOR FILING DATE: 2001-09-07
 PRIOR APPLICATION NUMBER: US60/318,130
 PRIOR FILING DATE: 2001-09-07
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 794
 SOFTWARE: Custom
 LENGTH: 257
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-236-392-28

Query Match 100.0%; Score 1073; DB 12; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-86;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCNGNPFVS 60
 DB 1 MAPAMESPTLLCVALFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCNGNPFVS 60
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSDDLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSDDLQASAE 120
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWNHNSITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWNHNSITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKA 197
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 4
 US-10-384-850-45
 Sequence 45, Application US/10384850
 Publication No. US20030175890A1
 GENERAL INFORMATION:
 APPLICANT: C. Fraser
 TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF
 FILE REFERENCE: 7853-217
 CURRENT APPLICATION NUMBER: US/10/384,850
 CURRENT FILING DATE: 2003-03-10
 PRIOR APPLICATION NUMBER: US/09/702,021
 PRIOR FILING DATE: 2000-10-30
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 45
 LENGTH: 257
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-384-850-45

Query Match 100.0%; Score 1073; DB 14; Length 257;
 Best Local Similarity 100.0%; Pred. No. 3.3e-86;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MAPAMESPTLLCVALFPAPDGLAVPQPKVSLNPPNRIKGENVTLTCNGNPFVS 60
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSDDLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGYKCOHQVNESEPVYLEVFSDDLQASAE 120

QY 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWNHNSITNATVEDSGTYCTGKV 180
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWNHNSITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKA 197
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 5
 US-09-944-277A-13
 Sequence 13, Application US/09944277A
 Patent No. US20020034771A1
 GENERAL INFORMATION:
 APPLICANT: Frank, Glenn R.
 Porter, James P.
 Rushlow, Keith E.
 Hassom, Donald L.
 TITLE OF INVENTION: Method to Detect IgE
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carol Talkington Verser, Ph.D.
 Heska Corporation
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: WordPerfect for Windows, Version 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/944,277A
 FILING DATE: 30-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/285,873
 FILING DATE: 1999-03-31
 ATTORNEY/AGENT INFORMATION:
 NAME: Verser, Carol Talkington
 REGISTRATION NUMBER: 37,459
 REFERENCE/DOCKET NUMBER: DI-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-7272
 TELEFAX: 970/484-9505
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 172 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-944-277A-13

Query Match 88.3%; Score 947; DB 9; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2.4e-75;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSSTKWFHNGSLSEETNSSLNINAKF 85
 DB 1 VPQPKVSLNPPNRIKGENVTLTCNGNPFVSSTKWFHNGSLSEETNSSLNINAKF 60
 QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMESQPLFLRCHGWRNDVYKVIY 145
 DB 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMESQPLFLRCHGWRNDVYKVIY 120
 QY 146 YKDGKALKYWNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
 DB 121 YKDGKALKYWNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

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RESULT 6
US-09-245-764-9
; Sequence 9, Application US/09245764
; Patent No. US20020107359A1
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245,764
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099,994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073,972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-764-9

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Best Local Similarity 100.0%; Pred. No. 2.4e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/09/245,764
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/099,994
; EARLIER FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: 60/073,972
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-245-764-9

Query Match      88.3%; Score 947; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.4e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 85
DB      1 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 60
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-4

Query Match      88.3%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.4e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 60
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/10/687,109
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-109-9

Query Match      88.3%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.4e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 85
DB      1 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 60
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF

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RESULT 8
US-10-687-109-9
; Sequence 9, Application US/10687109
; Publication No. US20040054480A1
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Maxwell, Kelly F.
; APPLICANT: Garrett, Thomas P.J.
; APPLICANT: Epa, Vidana
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF FC RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 4102-4
; CURRENT APPLICATION NUMBER: US/10/687,109
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 9
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-109-9

Query Match      88.3%; Score 947; DB 12; Length 172;
Best Local Similarity 100.0%; Pred. No. 2.4e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 85
DB      1 VPQKPKVSLNPPWNRIFKGENVTLCGNNFFVSSSTKWFHNGSLSEETNSLNIIVNAKF 60
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF

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FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-2

Query Match 88.3%; Score 947; DB 10; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.5e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85
Db 1 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 146 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 172

RESULT 10
US-10-293-992-2
; Sequence 2, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-992-2

Query Match 88.3%; Score 947; DB 12; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.5e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85
Db 1 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 146 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 172

RESULT 11

US-09-944-277A-6
; Sequence 6, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

Query Match 88.3%; Score 947; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.5e-75;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85
Db 1 VPQKPKVSLNPPWNRIFKGENVTITCNNGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 146 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 197
Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKQWOLDYSEPLNITVIKA 172

RESULT 12
US-09-809-715-4
; Sequence 4, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC

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; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE
; FILE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-715-4

Query Match      85.9%; Score 922; DB 10; Length 176;
Best Local Similarity 97.7%; Pred. No. 3.9e-73;
Matches 168; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      26 VPKPKVSLNPPWNRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSBETNSSLNINAKF 85
Db      1 VPKPKVSLNPPWNRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSBETNSSLNINAKF 60

QY      86 EDSGKYKQHOQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
Db      61 EDSGKYKQHOQVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120

QY      146 YKDGALKYWHNHNISITNATVDSGTYCTGKWLQDYSEPLNITVIKA 197
Db      121 YKDGALKYWHNHNISITNATVDSGTYCTGKWLQDYSEPLNITVIKA 172

RESULT 13
US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Crabtree, Julie
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Maiyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30

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; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 30
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-30

Query Match      78.3%; Score 840.5; DB 12; Length 218;
Best Local Similarity 80.2%; Pred. No. 7.4e-66;
Matches 158; Conservative 0; Mismatches 0; Indels 39; Gaps 1;

QY      1 MAPAMESPTLLCVALLFPDGVLAPOKPKVSLNPPWNRIFKGNVTLTCNGNFFVSS 60
Db      1 MAPAMESPTLLCVALLFPDGVLAPOKPKVSLNPPWNRIFKGNVTLTCNGNFFVSS 60

QY      61 STKWFHNGSLSEETNSNINAKFEDSGEYKQHQVNESEPVYLEVFSDDLLOASAE 120
Db      61 STKWFHNGSLSEETNSNINAKFEDSGEYK----- 92

QY      121 VMGQPLFLRCHGWRNWDVYKVIYKDGALKYWHNHNISITNATVDSGTYCTGKV 180
Db      93 -----CHGWRNWDVYKVIYKDGALKYWHNHNISITNATVDSGTYCTGKV 141

QY      181 WOLDYSEPLNITVIKA 197
Db      142 WOLDYSEPLNITVIKA 158

RESULT 14
US-10-434-817-12
; Sequence 12, Application US/10434817
; Publication No. US2003023579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA
; CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003

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; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 970/493-7272
;   TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 255 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
; MOLECULE TYPE: Protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-434-817-2

      Query Match          57.5%; Score 617; DB 15; Length 255;
      Best Local Similarity 60.2%; Pred.No. 3.9e-46;
      Matches 121; Conservative 24; Mismatches 52; Indels 4; Gaps 1;
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QY	1 MAPAMESPTLLCVALLFFAPGDGVLAVPQKPVKVSLNPPNNRIFKGENVTLTNGNNPFVS	60
Ddb	1 MPAPMGSPALLWITFLFSLDGVPAIRKSTVLSLNPPNNRIFRGENVTLTCKNKPLKN	60
	:	:
QY	61 STKWFNHGS;SEBETNSGLNVNAKPEDSGEYKCQHQQVNESEPVI LEVFSDMLLQSAAE	120
Ddb	: : :	:
QY	61 STEWTYNNTTTLEVVTSLSMTNASRRSGEYRCRNNDNLSEA VHLVEVFDMLLQSAAE	120
Ddb	: : : :	:
QY	121 VMWGQLFLURCHGWGNWDVKIVYYKGAEALKYWENHNISIT NATVEDSGETYCQG--	178
Ddb	: : : : :	:
QY	121 EVLEGKALVURCGWKDMDVFKVIYYKKGPLEYEWENKNI SIESATTENGSYTCCEGAF	180
Ddb	: : : : :	:
QY	179 --KWQLDYESEPLNITVIKA	197
Ddb	: : : : :	:
QY	181 NFXHTSERYS DYLNITVKA	201
Ddb	: : : : :	:

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Job time : 60.1562 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 10.7914 Seconds
(without alignments)
1756.007 Million cell updates/sec

Title: US-10-763-400-11
Perfect score: 1073
Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKVMQDYESBPLNITVIKA 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	257	2 S00682	IgE Fc receptor al
2	511	47.6	250	2 A34342	IgE Fc receptor al
3	489	45.6	245	2 A30154	IgE receptor alpha
4	405	37.7	296	2 I46021	Fc-gamma receptor
5	386.5	36.0	270	2 A34636	Fc-gamma receptor
6	373	35.3	404	2 A46480	Fc-gamma (19G) rec
7	376	35.0	344	2 A41357	Fc-gamma (19G) rec
8	376	35.0	374	1 A39878	Fc-gamma (19G) rec
9	375.5	35.0	280	2 I55577	Fc-gamma (19G) rec
10	373.5	34.8	336	2 I48471	Fc-gamma (19G) rec
11	367.5	34.2	254	1 JL0107	Fc-gamma (19G) rec
12	366	34.1	261	2 S29360	Fc-gamma (19G) rec
13	364.5	34.0	285	2 S36903	Fc-gamma (19G) rec
14	363.5	33.9	233	1 JU0284	Fc-gamma RIIB-alp
15	362	33.7	267	2 I56110	Fc-gamma (19G) rec
16	361.5	33.7	323	2 S06946	Fc-gamma (19G) rec
17	358	33.4	267	2 A35902	Fc-gamma (19G) rec
18	357.5	33.3	283	1 FCMSG1	Fc-gamma (19G) rec
19	357.5	33.3	310	2 JL0119	Fc-gamma (19G) rec
20	357.5	33.3	330	2 A40071	Fc-gamma (19G) rec
21	357.5	33.3	330	2 I49660	Fc-gamma-1/gamma-2
22	348	32.4	157	2 D31327	IgE receptor alpha
23	347	32.3	317	2 JL0118	Fc-gamma (19G) rec
24	343	32.0	267	2 I72882	Fc-gamma receptor
25	338	31.5	160	2 I47163	cytolytic trigger
26	220	20.5	159	2 I47164	cytolytic trigger
27	184.5	15.3	1694	2 S50065	sialoadhesin mou
28	156	14.5	104	2 I47165	cytolytic trigger
29	136.5	12.7	458	1 WMMSR1	biliary glycoprote

RESULT 1

S00682

IgE Fc receptor alpha chain precursor - human

N/Alternate names: Fc-epsilon receptor

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1988 #sequence, revision 31-Dec-1988 #text_change 23-Jul-1999

C/Accession: S00682; B30154; S42209

R/Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.

Nucleic Acids Res. 16, 3584, 1988

A/Title: Isolation of the gene coding for the alpha subunit of the human high affinity

A/Reference number: S00682; MUID:88233953; PMID:2967464

A/Accession: S00682

A/Molecule type: mRNA

A/Residues: 1-257 <KOC>

A/Cross-references: EMBL:X06948; NID:g31317; PIDN:CAA30025.1; PID:g31318

R/Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.

Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988

A/Title: Human and rat mast cell high-affinity immunoglobulin E receptors: Characterizat

A/Reference number: A94191; MUID:88158102; PMID:2964640

A/Accession: B30154

A/Molecule type: mRNA

A/Residues: 1-257 <SHI>

A/Cross-references: GB:J03605; NID:g187449; PIDN:AAA36204.1; PID:g307164

R/Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.

Eur. J. Biochem. 220, 593-598, 1994

A/Title: High-level expression of the truncated alpha chain of human high-affinity recei

nant product.

A/Reference number: S42209; MUID:94170811; PMID:8125119

A/Accession: S42209

A/Molecule type: protein

A/Residues: 26-197 <YAG>

A/Experimental source: purified recombinant protein

C/Genetics:

A/Gene: GDB:FCER1A

A/Cross-references: GDB:I19902; OMIM:147140

A/Map position: Iq23-Iq23

C/Superfamily: Fc gamma receptor III; immunoglobulin homology

C/Keywords: immunoglobulin receptor; transmembrane protein

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-257/Product: IGE Fc receptor alpha chain #status predicted <MAT>

F/44-95/Domain: immunoglobulin homology <IMM1>

F/125-178/Domain: immunoglobulin homology <IMM2>

Query Match

Best Local Similarity 100.0%; Score 1073; DB 2; Length 257;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVILTCNGNNFFEVS 60

Db 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRIKGENVILTCNGNNFFEVS 60

QY 61 STKWFHNGSLSETHSSLNINNAKFDSDGEYKQCQVNESEPVYLEVFSDWLLIQAAS 120

biliary glycoprote
biliary glycoprote
biliary glycoprote
elastic titin - hu
cell-adhesion mole
C-CAM2a protein is
ecto-ATPase presur
nonspecific cross-
vascular cell adhe
neuroglial - fruit
immunoglobulin-lik
macrophage colony-
FC gamma 2 recepto-
macrophage colony-
carcinoembryonic a
protein UNC-89 - C

Db	61	STKWFHNGLS	SETNSSLNI	VNA	FPDS	GEYK	QQVNE	SEPYL	EVFS	DMLL	QASAE	120
Qy	121	VVMGQP	FLR	CHGR	NRND	VKV	IYK	DGE	ALK	KWY	ENHN	ISIT
Db	121	VVMGQP	FLR	CHGR	NRND	VKV	IYK	DGE	ALK	KWY	ENHN	ISIT
Qy	181	WOLDYES	PLNT	TVIKA	197							
Db	181	WOLDYES	PLNT	TVIKA	197							

RESULT 2

A34342

IgE Fc receptor alpha chain precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Jun-1990 #sequence_revision

C/Accession: A34342; A61238

R/Ra, C.; Jouvin, M.H.E.; Kinet, J.P.

J. Biol. Chem. 264, 15323-15327, 1989

A/Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-R1) and

A/Reference number: A34342; MUID:89359361; PMID:2527850

A/Accession: A34342

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-250 <RAC>

A/Cross-references: GB:J05018; NID:G9193236; PIDN:AAA37600.1; PID:G9309224

R/Robertson, M.W.; Mehl, V.S.; Richards, M.L.; Liu, F.T.

Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991

A/Title: mRNA variants encoding multiple forms of the high-affinity IgE receptor alpha

A/Reference number: A61238; MUID:92234569; PMID:1839735

A/Accession: A61238

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 125-194 <RDB>

C/Superfamily: Fc gamma receptor III; immunoglobulin homology

C/Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein

F/42-94/Domain: immunoglobulin homology <IMM>

RESULT 3
A30154
IGF receptor alpha chain precursor - rat
N:Alternate names: Fc-epsilon-R alpha chain precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Oct-1989 #sequence revision 18-Oct-1989 #text_change 21-Jan-2000
C:Accession: C31327; A31327; A30154; A27116; I55304
R:Liou, F.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity IGF
A:Reference number: A94203; MUID:88289772; PMID:2969594
A:Accession: C31327
A:Molecule type: mRNA

A;Residues: 1-245 <LIU>
A;Cross-references: GB:M21622; GB:J03811
A;Experimental source: basophilic leukemia cell line, clone R3-4
A;Accession: A31327
A;Molecule type: mRNA
A;Residues: 21-245 <LI3>
A;Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811
A;Experimental source: basophilic leukemia cell line
R;Shimizu, A.; Repler, I.; Benfer, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A;Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization
A;Reference number: A94191; MUID:88158102; PMID:2964640
A;Accession: A30154
A;Molecule type: mRNA
A;Residues: 1-245 <SH1>
A;Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332
R;Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A;Title: A cDNA presumptively coding for the alpha subunit of the receptor with high affinity
A;Reference number: A27116; MUID:88024987; PMID:2959318
A;Accession: A27116
A;Molecule type: mRNA
A;Residues: 1, 'G', 3-235, 'N', 238-244, 'RLKPNS' <KIN>
R;Repler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A;Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structural
A;Reference number: I55304; MUID:89174653; PMID:2522441
A;Accession: I55304
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: GB:M23334; NID:G341335; PIDN:AAA74562.1; PID:G556391
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-245/Product: IgE receptor alpha chain #status predicted <MAT>
F;42-93/Domain: immunoglobulin homology #status predicted <IMM>

RESULT 4
I46021
Fc-gamma receptor II - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
C:Accession: I46021; S40204
R:Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A:Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
A:Reference number: I46021; MUID:94245284; PMID:8188320
A:Accession: I46021
A:Status: preliminary; translated from GE/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-296 <Zhang>

A; Cross-references: EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G437979
C; Superfamily: Fc gamma receptor II; immunoglobulin homology
C; Keywords: immunoglobulin receptor

	Query Match	37.7%	Score 405;	DB 2;	Length 296;
	Best Local Similarity	42.2%	Pred. No. 3.9e-25;		
	Matches	79;	Conservative	33;	Mismatches 71; Indels 4; Gaps 2
QY	10	LLCVALLFPADGVLAVPQPKP	-VSLPPPNRIKGENVLTTCNGNTPFEVSSTKWFHN	67	
DB	29	LWLTALLFLAP	-VSGKEDLPKAVVTIQPAWNLVLRDHVTLTCQGTSPSAGNLTTWFHN	86	
QY	68	GSLSEETNSLNIYNAKFDSEGEYKCOHQVNESEPVLEVPFSDWLLLCASREVVMGEOP	127		
DB	87	GSIIHTQQPSYSPFAGNSDSSGRQREQTSJDPVHLDDVLSDWLLLTQTPSLVFCGEFP	146		
QY	128	LFRLCHGWNRNDVYKVIYKQGEALKQWYENHNHISITNATVDSGGYCYCTGKWQLDYES	187		
DB	147	IMLRCHSWRNQPLNKKITFYQKRKISFYQRTNFSIPRNLHSGQYHCTAFIGKMLHSS	206		
QY	189	EPLNTY	194		
DB	207	QPVNTY	213		

RESULT 5
A34636
FC-gamma receptor II precursor - guinea pig
C:Species: *Cavia porcellus* (Guinea pig)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C:Accession: A34636
R:Tominaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A:Title: The structure and expression of the guinea pig FC receptor for IgG1 and IgG2 (H
A:Reference number: A34636; MUID:90241239; PMID:1692213
A:Accession: A34636
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <DOM>
A:Cross-references: GS:M35272
C:Superfamily: FC gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor
F:/37-88/Domain: immunoglobulin homology <IM>

Query Match	36.0%	Score	386.5	DB 2	Length	270			
Best Local Similarity	43.5%	Pred. No.	1.1e-23						
Matches	81	Conservative	23	Mismatches	81	Indels	1	Gaps	1
Qy	10	LLCVALFFAP-DGVLAVPQPKVSLNPPNMRIFKGENVTILTCGNNGFFVFSSTKWFHG	68						
Db	2	LLMTVLFLAPVAGTSADPPKAVVRLPEPMIQVLGRDVTULTCEGAPSPGNHSTOWLHG	61						
Qy	69	SLSEETNSSLNINAKEDSGEYKCOHQVNSEFPVYLEVPSDMLLQASAEVMEGQPL	128						
Db	62	RLIPTQVLPSYRFTAKGNDSGEYRCQAGGTSLSDPVLVDISDWLVLQTSOLIFQEGDVI	121						
Qy	129	FLRCHGRNDVYKVIYKDGAEALKYVENHNIITNATVDSGTYCTGKVMQDYESE	188						
Db	122	VLRCHSNNWPLAKVTFYHNGVAKYYSISKWPSIQANHSHSGAYNCTGLIGRTSHSP	181						
Qy	189	PLNITY	194						
Db	182	PVTITY	187						

RESULT 6
A46480
Pc gamma (IgG) receptor high affinity - mouse
N_AlterName: high affinity IgG receptor
C_Species: Mus musculus (house mouse)
C_Date: 18-Jun-1993 #sequence_revision
C_Accession: A46480; A43511
R_Organism: N: Kozak, C.A.; McKenzie, I.F.; Hozarich, P.M.

J. Immunol. 148, 1570-1575, 1992

A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and

A;Reference number: A46480; MUID:92166399; PMID:1531670

A;Accession: A46480

A;Status: Preliminary

A;Molecule type: DNA

A;Residues: 1-404 <OSM>

A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC

R;Seas, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.

J. Immunol. 144, 371-378, 1990

A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgC

A;Reference number: A43511; MUID:90111035; PMID:2136886

A;Accession: A43511

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-404 <SEA>

A;Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753

C;Superfamily: Fc gamma receptor I; immunoglobulin homology

C;Keywords: immunoglobulin receptor; transmembrane protein

F;127-179/Domain: immunoglobulin homology <IMM>

Query Match	35.3%;	Score 379;	DB 2;	Length 404;
Best Local Similarity	41.8%;	Pred. No. 6.7e-23;		
Matches	77;	Conservative	37;	Mismatches 69; Indels 2; Gaps 2;
QY	10	LLCVALLFPADGLVAVPQPKVYSLNPPNRRIFKGENVLTTCNGNNFFVSVSTKFWPHNGS	69	
DB	12	LLTTLJLVPGGVYVNAKAVITLQPPVSIQFQENVTLCBGPGLPGDSQTQWFINGT	71	
QY	70	LSEETNSSLNINAKFEDGEYKCOHQVNESEPPVLEVPFDWLLLCASAEVVMGQPLF	129	
DB	72	AVOISTFSYSIPEASFQDSGEYRCQTGSSMPSPFVLQIHNDMLLCASRRVLTEGEPLA	131	
QY	130	LRCHGRNDDVYKVIYKKDGEALKYVWENHNISITNATVEDSDSYTCTGKVMQLDYSESP	189	
DB	132	LRCHGWKLVVNVYVRNCKSPQFSSDSEVALLTNLSHSGIYHCSGTGRHRTVSAG	189	
QY	190	LNITV	194	
DB	190	VSITV	194	

RESULT 7

A41357 Fc gamma (IgG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jan-2000
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; UID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL1>
A;Cross-references: GB:X41355; GB:M21090; NID:G31333; PIDN:CAA32536.1; PID:G31334
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc
A;Reference number: S03018; UID:89098339; PMID:297497
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL2>
A;Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334
A;Note: The authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
P;117-170/Domain; immunoglobulin homology <IMM>

Query Match	35.0%	Score 376;	DB 2;	Length 344;
Best Local Similarity	39.7%;	Pred. No. 9.7e-23;		
Matches	73;	Conservative	39;	Mismatches 70;
				Indels 2;
				Gaps 2;

C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane

F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-292/Domain: extracellular #status predicted <EXT>
F;117-170/Domain: immunoglobulin homology <IMM2>
F;293-313/Domain: transmembrane #status predicted <TMW>
F;59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 376; DB 1; Length 374;
Best Local Similarity 39.7%; Pred. No. 1.1e-22;
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGLAVPQPKVSKVSNPPWNRIFKGENVTLTGNNFFEVSTKQWFHNSGL 70
DB 4 LTTLLLVWVVDGQVDT-TKAVITLQPPWVSVFQEEVTILHCEVLHLPQSSSTQWFLNGTA 62

QY 71 SEETNSSLNINNAKPEDSGEYKCOHQQVNESBPVYLEVFSDWLLLQASAEVVMGQPLFL 130
DB 63 TOTSPSYRITASVNDSEYRCQGLSGRSDPQLQLEIHRGWLMLLQVSSRVFMEGEPLAL 122

QY 131 RCHGHRNWDVYKVIYKQGEALKYVNNHNSITNATVEDSGTYTCTGKVWOLDYSEBPL 190
DB 123 RCHAWKDKLVNLYIRNGAKFPHWNSNLTKTNISHNGTYHCSG-MGKHRTTSAGI 181

QY 191 NITV 194
DB 182 SVTV 185

RESULT 9
FC gamma (IgG) receptor I-B splice form 1 precursor - human
N;Alternate names: CD64
N;Contains: Fc-gamma (IgG) receptor I-B splice form 2
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I55577; I70303
R;Peres, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.B.; Kimberly, R.P.
J. Clin. Invest. 90, 2102-2109, 1992
A;Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A;Reference number: I55577; MUID:93055454; PMID:1430234
A;Accession: I55577
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-280 <RES>
A;Cross-references: GB:L03419; NID:g182460; PIDN:AAA35825.1; PID:g292023
A;Note: splice form B1
A;Accession: I70303
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-10,103-153, 'A',155-280 <RE2>
A;Cross-references: GB:L03420; NID:g182461; PIDN:AAA35826.1; PID:g292024
A;Experimental source: mononuclear cells
A;Note: splice form B2
C;Comment: This receptor does not bind monomeric IgG with high affinity.
C;Genetics:
A;Gene: GDB:FCGR1B; CD64
A;Cross-references: GDB:35923; OMIM:601502
A;Map position: lp12-1p12
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
F;117-170/Domain: immunoglobulin homology <IMW>

Query Match 35.0%; Score 375.5; DB 2; Length 280;
Best Local Similarity 41.7%; Pred. No. 8.4e-23;
Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGLAVPQPKVSKVSNPPWNRIFKGENVTLTGNNFFEVSTKQWFHNSGL 70
DB 4 LTTLLLVWVVDGQVDT-TKAVITLQPPWVSVFQEEVTILHCEVLHLPQSSSTQWFLNGTA 62

QY 71 SEETNSSLNINNAKPEDSGEYKCOHQQVNESBPVYLEVFSDWLLLQASAEVVMGQPLFL 130
DB 63 TOTSPSYRITASVNDSEYRCQGLSGRSDPQLQLEIHRGWLMLLQVSSRVFMEGEPLAL 122

A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phospho-anchored isoforms

A;Reference number: A32933; MUID:89296947; PMID:2525780

A;Accession: A32933

A;Molecule type: mRNA

A;Residues: 31-254 <CA>

A;Cross-references: GB:M24853; NID:g184849; PIDN:AAA53506.1; PID:G386806

R;Gasser, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.

J. Biol. Chem. 270, 1350-1361, 1995

A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole

A;Reference number: A55439; MUID:95138131; PMID:7836402

A;Accession: I37627

A;Molecule type: DNA

A;Residues: 1-39 <RES>

A;Cross-references: EMBL:Z46222; NID:G559445; PIDN:CAA86295.1; PID:g1478198

A;Note: translation has been corrected relative to PID:g871305

C;Comment: This low affinity Igg Fc receptor of natural killer cells, which is the product of a gene nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in

C;Genetics:

A;Gene: GDB:FCGR3A; FCGR3

A;Cross-references: GDB:119904; OMIM:146740

A;Map position: 1q23-1q23

A;Introns: 14/1; 21/1

A;Note: the list of introns is incomplete

C;Superfamily: Fc gamma receptor III; immunoglobulin homology

C;Keywords: glycoprotein; receptor; transmembrane protein

F:11-17/Domain: signal sequence #status predicted <SIG>

F:18-254/Product: Fc gamma (Igg) receptor III-A #status experimental <MAT>

F:18-208/Domain: extracellular #status predicted <EXT>

F:40-91/Domain: immunoglobulin homology <IMM1>

F:111-174/Domain: immunoglobulin homology <IMM2>

F:209-229/Domain: transmembrane #status predicted <TR>

F:230-254/Domain: intracellular #status predicted <CYT>

F:556.63.92.180.187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.2%; Score 367.5; DB 1; Length 254;

Best Local Similarity 42.8%; Pred. No. 3.3e-22;

Matches 80; Conservative 27; Mismatches 77; Indels 3; Gaps 2;

QY 10 LLCVALLFPADGVLAVPQPK--VSLNPWNRIFKGENVTILTCNGNNFEVSGTKWFHN 67

DB 5 LLPTALLLLVSAG-MRTEDLPKAVVFLPEQWYRVLEKDSVTLKCCGAYSPEINSTQWFHN 63

QY 68 GSLSEETSSNLINVAKFSDSGEYKCOHQOVNESEPVYLEVFSDDLQLLQASAEVYMBGQP 127

DB 64 ESLISSQASSYFIDAATVDDSDSEYRCOTNLSTLSDPVQLVHIGWLLLAQPRWFKEDP 123

QY 128 LFLRCHGNRWNDYKVIYVYKGEALKYWYENHNISITNATVDSGYTYCTGKVMQLDYES 187

DB 124 IHLRCHSWKNTALHKVTYLQNGKGRKYFHNSDFYIPKATLKDSGSYFCRGLFGSKNVSS 183

QY 188 EPLNITV 194

DB 184 ETVNITI 190

RESULT 12

S29360

Fc gamma (Igg) receptor alpha - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S29360; S46999

R;Ravetch, J.V.; Luster, A.D.; Weishank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; I

Science 234, 718-725, 1986

A;Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc :

A;Reference number: S29360; MUID:87042761; PMID:2946078

A;Accession: S29360

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-261 <RA>

A;Cross-references: EMBL:M14215; NID:g193247; PIDN:AAA37604.1; PID:g309228

R;Feinman, R.; Qiu, W.Q.; Pearce, R.N.; Nikolaiczky, B.S.; Sen, R.; Sheffery, M.; Ravet

EMBO J. 13, 3852-3860, 1994

A;Title: PU.1 and an HLH family member contribute to the myeloid-specific transcription

A:Reference number: S46999; MUID:94349933; PMID:8070412

A:Accession: S46999

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <PEI>

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor; transmembrane protein

F:130-183/Domain: immunoglobulin homology <IMM2>

Query Match 34.1%; Score 366; DB 2; Length 261;

Best Local Similarity 40.5%; Pred. No. 4.4e-22;

Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGVAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNG-S 69

DB 16 LTILLFAPDRQSAALPKAVVLLDPPIQVLKEDMTLMCEGTHNPGNSSTQWFHNGS 75

QY 70 LSEETNSLINVAKFSDSGEYKQCHQVNESEPVYLEVFSDFDMLLIQASAEVVMGQPLF 129

DB 76 IRSQWQASYTF-KATVNDSGEYRCQMEQTRUSDPLDGLVSDMLLOTQPVFLEGETIT 134

QY 130 LRCHGWRNDVYKVIYKDGALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSESP 189

DB 135 LRCHSWRNKLNIRISFFHNESVRVHYKSNFSIPKANSHSGDYCKGSLGSGTQHQSKP 194

QY 190 LNIIV 194

DB 195 VTITV 199

RESULT 13

Fc gamma (IgG) receptor type 2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

A:Accession: S36903

R:Bocek, P.; Pecht, I.

FEBS Lett. 331, 86-90, 1993

A:Title: Cloning and sequence of the cDNA coding for rat type II Fc-gamma receptor of ma

A:Reference number: S36903; MUID:94009652; PMID:8405417

A:Accession: S36903

A:Molecule type: mRNA

A:Residues: 1-285 <BOC>

A:Cross-references: EMBL:X73371; NID:9397576; PIDN:CAA51788.1; PID:9397577

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor

F:52-103/Domain: immunoglobulin homology <IMM>

Query Match 34.0%; Score 364.5; DB 2; Length 285;

Best Local Similarity 38.9%; Pred. No. 6.5e-22;

Matches 72; Conservative 36; Mismatches 76; Indels 1; Gaps 1;

QY 10 LLCVALFFAPDGVAVPQPKVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNGS 69

DB 19 LLWTAVLNVAESHAGLP-KAVVXLEPPWIQVLKEDTTLTLMCEGTHNPKNCSTQWFHNGS 77

QY 70 LSEETNSLINVAKFSDSGEYKQCHQVNESEPVYLEVFSDFDMLLIQASAEVVMGQPLF 129

DB 78 SIWHAQANYTFKATVNDSGEYRCMEETGISEPIHLGLVSDMLLOTQSLVFEGETIT 137

QY 130 LRCHGWRNDVYKVIYKDGALKYWYENHNISITNATVEDSGTYTCTGKWQLDYSESP 189

DB 138 LRCHSWRNKLNIRISFFHNESVRVHYKSNFSIPKANSHSGDYCKGSLGSGTQHQSKP 197

QY 190 LNIIV 194

DB 198 VTITV 202

RESULT 14

Fc gamma (IgG) receptor III-B precursor (neutrophil) - human

N:Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra

C:Species: Homo sapiens (man)

C>Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 28-Jan-2000

C:Accession: JU0284; S00758; I37628; B32933; A31460

R:Ravetch, J.V.; Perussia, B.

J. Exp. Med. 170, 481-497, 1989

A:Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cells

A:Reference number: JLO107; MUID:89328325; PMID:2526946

A:Accession: JU0284

A:Molecule type: mRNA

A:Residues: 1-201, 'SF', 204-233 <RAV>

A:Cross-references: GB:J04162

A:Note: the sequence of the receptor from human NK cells, reported in the same paper, di

rboxyl end

R:Simmons, D.; Seed, B.

Nature 333, 568-570, 1988

A:Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane

A:Reference number: S00758; MUID:88232937; PMID:2967436

A:Accession: S00758

A:Molecule type: mRNA

A:Residues: 1-233 <SIM>

A:Cross-references: EMBL:X07934; NID:929744; PIDN:CAA30758.1; PID:929745

R:Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.

J. Biol. Chem. 270, 1350-1361, 1995

A:Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole

A:Reference number: A55439; MUID:95138331; PMID:7836402

A:Accession: I37628

A:Molecule type: DNA

A:Residues: 1-72 <RES>

A:Cross-references: EMBL:Z46223; NID:9559446; PIDN:CAA86296.1; PID:9871306

R:Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C

Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989

A:Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph

A:Reference number: A32933; MUID:89296947; PMID:2525780

A:Accession: B32933

A:Molecule type: mRNA

A:Residues: 1-121, 'E', 123-150, 'S', 152-233 <SCA>

A:Cross-references: GB:M24854; NID:9184851; PIDN:AAA53507.1; PID:9306930

R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.

Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989

A:Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal

A:Reference number: A31460; MUID:89128838; PMID:2521732

A:Accession: A31460

A:Molecule type: mRNA

A:Residues: 1-35, 'R', 37-64, 'N', 66-81, 'D', 83-105, 'V', 107-233 <PEL>

A:Cross-references: GB:J04162; NID:9183036; PIDN:AAA35881.1; PID:9183037

C:Comment: this low affinity IgG Fc receptor of neutrophils, which is the product of the

1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod

C:Genetics:

A:Gene: GDB:FCGR3B; FCG3; FCGR3

A:Cross-references: GDB:128176; OMIM:146740

A:Map position: 1Q23-1Q23

A:Introns: 14/1, 21/1

C:Note: the list of introns is incomplete

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag

F:1-16/Domain: signal sequence #status predicted <SIG>

F:19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>

F:40-91/Domain: immunoglobulin homology <IMM1>

F:111-174/Domain: immunoglobulin homology <IMM2>

F:5663,82,92,180,187/Binding site: carbohydrate (asn) (covalent) #status predicted

F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 33.9%; Score 363.5; DB 1; Length 233;

Best Local Similarity 42.8%; Pred. No. 6.2e-22;

Matches 80; Conservative 26; Mismatches 78; Indels 3; Gaps 2;

QY 10 LLCVALFFAPDGVAVPQPKK--VSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNG 67

DB 5 LLPTALLLVASG-MRTEDLPKAVVLEPQWYSVLEKDSVTLKCCQGAYSPEDNSTQWFHNG 63

QY 68 GSLSEETNSLINVAKFSDSGEYKQCHQVNESEPVYLEVFSDFDMLLIQASAEVVMGQPL 127

DB 64 ESLISSQASSYFIDAATVNDSGEYRCQTNLTSLSDPVLQLEVHICWLLQLQAPRWVFEKEDP 123

QY 128 LFLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWOLDYES 187
Db 124 IHLRCHSWKNTALHKVYIQLNGKDRKYFHHNSDFHPRATLKDSGSYFCRGLVGSKNVSS 183
QY 188 EPLNITV 194
Db 184 ETVNITI 190

RESULT 15
I56110
Fc-gamma RIIB-alpha - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C:Accession: I56110
R:Farber, D.L.; Sears, D.W.
J:Immunol. 146, 4352-4361, 1991
A:Title: Rat Cdi6 is defined by a family of class III Fc-gamma receptors requiring co-ex
A:Reference number: I56110; MUID:91250730; PMID:1710249
A:Accession: I56110
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267 <RES>
A:Cross-references: GB:M64369; NID:G206674; PIDN:AAA42048.1; PID:G206675
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
F:55-106/Domain: immunoglobulin homology <IMM>

Query Match 33.7%; Score 362; DB 2; Length 267;
Best Local Similarity 39.7%; Pred. No. 9.5e-22;
Matches 73; Conservative 34; Mismatches 77; Indels 0; Gaps 0;
QY 11 LCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNPFVSVSTKWFHNSL 70
Db 22 LTMLLLFAPADROTANLPKAVVRDPPWIOVLKEDVTITCEGTHNPGNSSQWFHNS 81
QY 71 SEETNSLNIIVNAKFEDSGEYKQHQVNESEFVYLEVFSDFWLLQASAEVWMEGQPLFL 130
Db 82 TWGQVQASYTFKATVNDSGEYRCMAHTSLSDPIHLEVISDWLLLTLPQVFEGETITL 141
QY 131 RCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWOLDYSEPL 190
Db 142 RCHSWKNKQLTKVLLFQNGKPRVYYQSSNFSIPKANHSHSGNYCKAYILGRTHVSKPV 201
QY 191 NITV 194
Db 202 TITV 205

Search completed: October 6, 2004, 09:23:43
Job time : 11.7914 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 6.65851 Seconds
(without alignments)
1540.558 Million cell updates/sec

Title: US-10-763-400-11

Perfect score: 1073
Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKWLQDYSEPLNITVIKA 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	257	1 FCEA_HUMAN	P12319 homo sapien
2	511	47.6	250	1 FCEA_MOUSE	P20489 mus musculus
3	489	45.6	245	1 FCE1_RAT	P12371 rattus norv
4	405	37.7	296	1 FCG2_BOVIN	Q28110 bos taurus
5	387.5	36.1	341	1 FCG2_CAVPO	Q60513 cavia porce
6	379	35.3	374	1 FCG1_HUMAN	P12314 homo sapien
7	379	35.3	404	1 FCG1_MOUSE	P26151 mus musculus
8	368.5	34.3	250	1 FCG3_BOVIN	P79107 bos taurus
9	368	34.3	257	1 FCG3_PIG	Q28942 sus scrofa
10	367.5	34.2	254	1 FCG3_HUMAN	P08637 homo sapien
11	366	34.1	261	1 FCG3_MOUSE	P08508 mus musculus
12	364.5	34.0	285	1 FCG2_RAT	Q63203 rattus norv
13	363.5	33.9	233	1 FCG3_HUMAN	O75015 homo sapien
14	363	33.8	267	1 FCG3_RAT	P27845 rattus norv
15	361.5	33.7	310	1 FCG3_HUMAN	P31994 homo sapien
16	361.5	33.7	323	1 FCGC_HUMAN	P31995 homo sapien
17	357.5	33.3	330	1 FCG2_MOUSE	P08101 mus musculus
18	348.5	32.5	316	1 FCGA_PANTR	Q8SPV8 pan troglod
19	348	32.4	157	1 FCE2_RAT	P12840 rattus norv
20	347	32.3	317	1 FCGA_HUMAN	P12318 homo sapien
21	172	16.0	1709	1 SN_HUMAN	Q9B222 homo sapien
22	164.5	15.3	1694	1 SN_MOUSE	Q62230 mus musculus
23	152	14.2	422	1 K3L1_RAT	P83556 rattus norv
24	144	13.4	432	1 K3L1_MOUSE	P83555 mus musculus
25	136.5	12.7	521	1 CEAL_MOUSE	P31809 mus musculus
26	135	12.6	837	1 NCM2_MOUSE	Q35136 mus musculus
27	130	12.1	519	1 ECTO_RAT	P16573 rattus norv
28	128.5	12.0	344	1 CEAC_HUMAN	P40199 homo sapien
29	126.5	11.8	1302	1 NRG_DROME	P20241 drosophila
30	125.5	11.7	978	1 KFMS_RAT	Q00495 rattus norv
31	124.5	11.6	977	1 KFMS_MOUSE	P09581 mus musculus
32	120	11.2	702	1 CEAS_HUMAN	P06731 homo sapien
33	120	11.2	6632	1 UN89_CAEEL	O01751 caenorhabdi

34 118 11.0 458 1 CD4_MACNE
35 117.5 11.0 837 1 NCM2_HUMAN
36 117.5 11.0 847 1 CD22_HUMAN
37 117 10.9 1197 1 CAM1_BRARE
38 116 10.8 458 1 CD4_CERAB
39 116 10.8 1240 1 NFAS_HUMAN
40 116 10.8 3707 1 FGBM_MOUSE
41 114.5 10.7 344 1 NTRI_HUMAN
42 114.5 10.7 344 1 NTRI_MOUSE
43 114.5 10.7 344 1 NTRI_RAT
44 113.5 10.6 1021 1 CONT_RAT
45 113 10.5 458 1 CD4_MACPA

ALIGNMENTS

RESULT 1
FCEA_HUMAN
ID_FCEA_HUMAN STANDARD; PRT; 257 AA.
AC P12319;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCER1) (Ige Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).
GN FCER1A OR FCE1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88233953; PubMed=2967464;
RA Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;
RT "Isolation of the gene coding for the alpha subunit of the human high
RT affinity Ige receptor.";
RL Nucleic Acids Res. 16:3584-3584(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Maat cells;
RX MEDLINE=88158102; PubMed=2964640;
RA Shimizu A., Repler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-197.
RX MEDLINE=93113350; PubMed=1472946;
RA Padlan E.A., Helm B.A.;
RT "A modeling study of the alpha-subunit of human high-affinity
RT receptor for immunoglobulin-E.";
Receptor 2:129-144(1992).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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DR EMBL; X06948; CAA30025.1; -
 DR EMBL; J03605; AAA36204.1; -
 DR EMBL; A21606; CRA01564.1; -
 DR PIR; S00682; S00682.
 DR PDB; 1ALS; 27-FEB-95.
 DR PDB; 1ALT; 27-FEB-95.
 DR PDB; 1F2Q; 08-JUN-00.
 DR PDB; 1J86; 29-AUG-01.
 DR PDB; 1J87; 29-AUG-01.
 DR PDB; 1J88; 29-AUG-01.
 DR PDB; 1J89; 05-SEP-01.
 DR Genew; HGNC:3609; FCER1A.
 DR MIM; 147140; -
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00408; Igc2; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; 3D-structure.
 FT SIGNAL 1 25
 FT CHAIN 26 257
 FT HIGH AFFINITY IMMUNOGLOBULIN EPSILON
 FT RECEPTOR ALPHA-SUBUNIT
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE 1.
 FT DOMAIN 30 110
 FT DOMAIN 111 193
 FT DISULFID 51 93
 FT DISULFID 132 176
 FT CARBOHYD 46 46
 FT CARBOHYD 67 67
 FT CARBOHYD 75 75
 FT CARBOHYD 99 99
 FT CARBOHYD 160 160
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT STRAND 31 35
 FT HELIX 39 42
 FT TURN 43 43
 FT STRAND 48 54
 FT STRAND 61 66
 FT TURN 67 68
 FT STRAND 69 71
 FT STRAND 74 74
 FT TURN 75 76
 FT STRAND 77 79
 FT HELIX 82 87
 FT STRAND 91 96
 FT HELIX 98 100
 FT TURN 101 101
 FT STRAND 104 107
 FT STRAND 114 116
 FT HELIX 120 124
 FT STRAND 128 133
 FT STRAND 143 145
 FT STRAND 146 148
 FT TURN 149 149
 FT STRAND 150 150
 FT TURN 152 153
 FT STRAND 154 155
 FT TURN 156 159
 FT STRAND 160 163
 FT HELIX 165 170
 FT STRAND 175 178
 FT STRAND 181 182
 FT TURN 183 185
 FT STRAND 186 187
 FT STRAND 190 193
 SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;

Query Match

100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.5e-86;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFFEVS 60
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFFEVS 60
 QY 61 STKWFHNGSLSEETNSSLNINNAKFDSEGYKCHQCVNESEPVYLEVFSWMLLQASAE 120
 DB 61 STKWFHNGSLSEETNSSLNINNAKFDSEGYKCHQCVNESEPVYLEVFSWMLLQASAE 120
 QY 121 VMNEGQPLFRCHGWRNWDVYKVIYKDGALKYWYENHNSITNATVEDSGTYCTGKV 180
 DB 121 VMNEGQPLFRCHGWRNWDVYKVIYKDGALKYWYENHNSITNATVEDSGTYCTGKV 180
 QY 181 WOLDYSEPLNITVIKA 197
 DB 181 WOLDYSEPLNITVIKA 197
 RESULT 2
 FCEA MOUSE STANDARD; PRT; 250 AA.
 ID FCEA MOUSE
 AC P20489;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
 GN FCER1A OR FCE1A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359361; PubMed=2527850;
 RA Ra C., Jouvain M.H.E., Kinet J.-P.;
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc
 epsilon RI) and surface expression of chimeric receptors
 RT (rat-mouse-human) on transfected cells.";
 RL J. Biol. Chem. 264:15323-15327(1989).
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
 CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
 CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
 CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
 CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
 CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
 CC DISULFIDE LINKED GAMMA CHAINS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
 CC
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 CC
 CC EMBL; J05018; AAA37600.1; -
 CC PIR; A34342; A34342.
 CC HSSP; P12319; 1ALS.
 CC MGD; MGI:95494; Fcer1a.
 CC GO; GO:0007185; P:signal transduction; IDA.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; Ig.
 CC Pfam; PF00047; ig; 2.
 CC SMART; SM00409; IG; 2.
 CC PROSITE; PS50835; IG_LIKE; 1.
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.

```
FT SIGNAL 1 23
FT CHAIN 24 250
FT DOMAIN 24 204
FT TRANSMEM 205 223
FT DOMAIN 224 250
FT DOMAIN 28 104
FT DOMAIN 114 181
FT DISULFID 49 92
FT DISULFID 131 174
FT CARBOHYD 58 58
FT CARBOHYD 66 66
FT CARBOHYD 73 73
FT CARBOHYD 106 106
FT CARBOHYD 152 152
FT CARBOHYD 167 167
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BFB4DC0C4E CRC64;

Query Match 47.6%; Score 511; DB 1; Length 250;
Best Local Similarity 51.1%; Pred. No. 1.5e-37;
Matches 96; Conservative 38; Mismatches 52; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGVAVPQKPVSLNPPWIRFKGENTLTCNGNFFEV-SSTKWFHNGS 69
Db 9 LCLALLFMSLDVILFATEKSVLTLDPPWIRIFTEGKVTLSYGNHQLQMNSTTKWIHNGT 68
QY 70 LSEETNSLINVNAKFEDSGYKCOHQOVNESEPVYLEVFSMDLLQLQASAEVVMGQPLF 129
Db 69 VSEVNSSHLVVSATVDSQGYKCOQKGLFKSKPVLYNVQDWLLLTSDADMLVHGSEF 128
QY 130 LECHGRWYDVKYIYKDGALKYWHNHNISITNATVDSGYTCYKQWQLDYSEPL 189
Db 129 IRCHGKNNVRKVIYRDNHAFNYSVES-PVSIREATLNDSGTYHCKYLRQVYESDK 187
QY 190 LNIITVKA 197
Db 188 FRIAVVKA 195
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RESULT 3
ID FCEI RAT STANDARD; PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCRI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN FCRI OR FCRI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakimi J., Kochan J.;
RT "A cDNA presumptively coding for the alpha subunit of the receptor
RT with affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RN [2]
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Test cells;
RX MEDLINE=88158102; PubMed=2964540;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
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RN RP SEQUENCE OF 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;
RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IgE receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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CC or send an email to license@sb-sib.ch).
CC
CC EMBL; M17153; AAA42045.1; -
CC EMBL; J03606; AAA41582.1; -
CC EMBL; M21822; AAA41146.1; -
CC FIR; C31327; A30154.
CC HSP; P12319; IALS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003599; IG.
CC DR Pfam; PF00047; Ig; 2.
CC DR SMART; SM00409; IG; 2.
CC DR PROSITE; PS50835; IG LIKE; 1.
CC IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 245
FT DOMAIN 24 204
FT TRANSMEM 205 223
FT DOMAIN 224 245
FT DOMAIN 28 103
FT DOMAIN 113 181
FT DISULFID 49 91
FT DISULFID 130 174
FT CARBOHYD 52 52
FT CARBOHYD 53 53
FT CARBOHYD 58 58
FT CARBOHYD 65 65
FT CARBOHYD 123 123
FT CARBOHYD 158 158
FT CARBOHYD 167 167
SQ SEQUENCE 245 AA; 27793 MW; A0E67DD363B72197 CRC64;

Query Match 45.6%; Score 489; DB 1; Length 245;
Best Local Similarity 48.9%; Pred. No. 1.2e-35;
Matches 91; Conservative 37; Mismatches 58; Indels 0; Gaps 0;

QY 11 LCVALFFAPDGVAVPQKPVSLNPPWIRFKGENTLTCNGNFFEV-SSTKWFHNGSL 70
Db 9 LCLALVLSLGVMLTATQKWSLDPFWIRLTGDKVTLCNGNNSOMNKTWINDSI 68
QY 71 SEETNSLINVNAKFEDSGYKCOHQOVNESEPVYLEVFSMDLLQLQASAEVVMGQPLF 130
Db 69 SNVSKSHWVVSATIQSGKIICQKGFYKSKPVLYNVQDWLLQSSADVVDNGSPDI 128
QY 131 RCHGRWYDVKYIYKDGALKYWHNHNISITNATVDSGYTCYKQWQLDYSEPL 190
Db 129 RCRSKWKVKYIYKDDIAFKYSYDSNNISIRKATFNDSGSYHCTGYLNKVECKSKF 188
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QY 191 NITV1K 196
Db 189 SIATVK 194

RESULT 4
FCG2_BOVIN STANDARD; PRT; 296 AA.
AC Q281LO:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-gamma RII) (FCRII) (IGG Fc receptor II).
GN FCGR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=94245284; PubMed=8189320;
RA Zhang G., Young J.R., Tregaskes C.R., Howard C.J.;
RL "Cattle Fc gamma RII: molecular cloning and ligand specificity."; Immunogenetics 39:423-427(1994).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Higher expression is found in macrophages than in neutrophils (Probable).
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of pPKN6/SHP-1.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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DR EMBL; X75671; CAAS3367.1; -.
DR PIR; I46021; I45021.
DR HSSP; P12319; 1ALS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; 1g; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
DR Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 42
FT CHAIN 43 296
FT REGION RECEPTOR II.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM
FT DOMAIN 226 246
FT DOVAIN 247 296
FT DOVAIN 247 296
FT DOVAIN 130 212
FT SITE 273 278
FT SITE 70 112
FT DISULFID 151 195
FT DISULFID 79 79
FT CARBOHYD 86 86
FT CARBOHYD 105 105
FT CARBOHYD 179 179
FT CARBOHYD 186 186
FT CARBOHYD 210 210

SO SEQUENCE 296 AA; 33020 MW; A61A40A611F71ED5 CRC64;
Query Match 37.7%; Score 405; DB 1; Length 296;
Best Local Similarity 42.2%; Pred. No. 3.3e-28;
Matches 79; Conservative 33; Mismatches 71; Indels 4; Gaps 2;
QY 10 LLCVALLFPAPDGVLAPOKPK--VSLNPPWNRIFKGENVILTCGNKPPFEVSSKWFHN 67
Db 29 LLWTALLFLAP--VSGKPLPKAVVTIQPAWNLVLRDEHVTLCQGTSTFSAGNLTWFHN 86
QY 68 GSLSEETSSNLVNAKPEDSGEYKQHQOVNESPVYLEVFSDWLLQLQASAEVVMGEP 127
Db 87 GSSIIHQKPSYFRAGNSDSYRCQREQTSLSDPVHLVDVSDWLLQLQTSLSLVEQGESE 146
QY 128 LFIKCHGRWNVYKVIYKQGEALKYWENHINISITATVEDSGTYCTGKVMOLDYES 187
Db 147 IMLRCHSWENQPLNKITFYQDRKSKIFSYQRTNFSIPRANLSHQYHCTAFIGKMLHSS 206
QY 188 EPLNITV 194
Db 207 QPWNITV 213

RESULT 5
FCG2_CAVPO STANDARD; PRT; 341 AA.
AC Q60513; Q60498; Q60511; Q60512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-gamma RII) (FCRII) (IGG Fc receptor II) (Fc-gamma-1/gamma-2 receptor).
GN FCGR2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=90241239; PubMed=1692213;
RA Tomimaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
RT "The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (Fc gamma 1/gamma 2R)."; Biochem. Biophys. Res. Commun. 168:683-689(1990).
RL Biochem. Biophys. Res. Commun. 168:683-689(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
RC STRAIN=JY-1;
RC MEDLINE=93346746; PubMed=8345193;
RA Yamashita T., Shinozaki K., Yamashita Y.;
RT "Expression cloning of complementary DNA encoding three distinct isoforms of guinea pig Fc receptor for IgG1 and IgG2."; J. Immunol. 151:2014-2023(1993).
RL J. Immunol. 151:2014-2023(1993).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=2R-B3;
CC IsoId=Q60513-1; Sequence=Displayed;
CC Name=2R-B1;
CC IsoId=Q60513-2; Sequence=VSP_002639;
CC Name=2R-B2;
CC IsoId=Q60513-3; Sequence=VSP_002638;
CC -!- TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes express preferentially isoform 2R-B1. B lymphocytes express isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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RA Collins R.A., Gelder K.I., Howard C.J.;
 RT "Nucleotide sequence of cattle FcγRIII: its identification in
 RL gammatdelta T cells."
 CC Immunogenetics 45:440-443(1997).
 CC -!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED
 CC OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-
 CC DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT
 CC ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X99695; CAA68026.1; -.
 CC HSP; P12319; IALS.
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF000047; Ig; 2.
 CC PROSITE; PS50835; IG_LIKE; 2.
 CC Igγ-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat; Polymorphism.
 FT SIGNAL 1 16
 FT CHAIN 17 250
 FT
 FT DOMAIN 17 208
 FT TRANSMEM 209 225
 FT DOMAIN 226 250
 FT DOMAIN 23 105
 FT DOMAIN 99 189
 FT DI-SULFID 47 89
 FT DI-SULFID 128 172
 FT CARBOHYD 56 56
 FT CARBOHYD 63 63
 FT CARBOHYD 180 180
 FT VARIANT 11 11
 FT VARIANT 12 12
 FT VARIANT 11 11
 FT VARIANT 107 107
 FT VARIANT 114 114
 FT VARIANT 229 229
 FT SEQUENCE 250 AA; 28050 MW; D625139E889E207 CRC64;
 SQ
 Query Match 34.3%; Score 368.5; DB 1; Length 250;
 Best Local Similarity 39.7%; Pred. No. 4.1e-25;
 Matches 77; Conservative 29; Mismatches 81; Indels 7; Gaps 1;
 Qy 1 MAPAMESFTLLCVALLFFADPGVLAVQKPKVSLNPPWNRIFKGVNLTCTGNNFEVS 60
 Db 4 LLPPAALFVLV-----SADTQTADPSKAVLLDPQNHVLTNDRVTLKCGDYPVEDN 56
 Qy 61 STKWFHNGSLSEETNSLNIWNAKFDSGEYKCOHQWNESEPVYLEVFSDDLQASAE 120
 Db 57 STKWHNGTLLISSPTPYFFADVKVQDSGEYKCTGTLSAPSDPKLVHVGWLLQVAQR 116
 Qy 121 VMEGQPLFLFCHGRNWDVVKVLYYKDGALKTKWYENHNISITNATVDSGYCTGKV 180
 Db 117 VNVGKPIRLKCHSKWKTTPAKVQYFRNGRGKYSHGNSDFHIPEAKLEHSGSYFCRGII 176
 Qy 181 WLDYSEPLNTIV 194
 Db 177 GSKNESSESVQITV 190

RESULT 9

FCG3_PIG

ID_FCG3_PIG STANDARD; PRT; 257 AA.

AC Q28942; Q28940; Q28941;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor
 DE (IGG Fc receptor III) (Fc-gamma RIII) (FcRIII) (Cytolytic trigger
 DE molecule G7).
 GN FCG3.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
 RC STRAIN=Minnesota miniature swine;
 RA MEDLINE=94358430; PubMed=8077673;
 RA Halloran P.J., Sweeney S.E., Strommeier C.M., Kim Y.B.;
 RT "Molecular cloning and identification of the porcine cytolytic
 RT trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue."
 RL J. Immunol. 153:2631-2641(1994).
 CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
 CC gamma. Low affinity receptor.
 CC -!- SUBUNIT: FORMS A COMPLEX WITH NK-E.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PMNC,
 CC MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
 CC THYMUS OR LIVER.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 CC
 CC EMBL; U08993; AAA57190.1; -.
 CC EMBL; U08991; AAA57188.1; -.
 CC EMBL; U08992; AAA57189.1; -.
 CC HSP; P12319; IALS.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC Pfam; PF000047; Ig; 2.
 CC SMART; SM00409; IG; 2.
 CC PROSITE; PS50835; IG_LIKE; 2.
 CC Igγ-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 19
 FT CHAIN 20 257
 FT
 FT DOMAIN 20 209
 FT TRANSMEM 210 230
 FT DOMAIN 231 257
 FT DOMAIN 25 104
 FT DOMAIN 108 190
 FT DI-SULFID 48 90
 FT DI-SULFID 129 173
 FT CARBOHYD 64 64
 FT CARBOHYD 134 134
 FT CARBOHYD 162 162
 FT CARBOHYD 181 181
 FT VARIANT 55 55
 FT VARIANT 149 149
 FT VARIANT 181 181
 FT VARIANT 186 186
 FT SEQUENCE 257 AA; 29062 MW; 1D038CC1552B97CB CRC64;
 SQ
 Query Match 34.3%; Score 368; DB 1; Length 257;
 Best Local Similarity 41.0%; Pred. No. 4.7e-25;
 Matches 77; Conservative 33; Mismatches 76; Indels 2; Gaps 1;

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QY 7 SPTLCVALLFPADGVLAPOKPKVSLNPNWRIKFGENVTLTCNGNNFEVSVSTRWFH 66
DB 6 SPTAL-LLLVSPGTHAEDPPKSVLLDPWDRLLKDSVTLCKQAGYPRDDSDSTWRW 63
QY 67 NGSLSSEETNSLNVNAKFEDESGYKQHQVNESEPVYLFVFSDWLLQLQSAEVMWEGQ 126
DB 64 NGLTISNKASSYSITDATVGNSEGYCTKTG-SAQSDPLRLVLYKGLWLLQAPRWVQGE 123
QY 127 PFLFRLCHGRWMDVYKVIYKDEGALKYWEHNHISITNATVEDSGTYCTGKVMQLDYE 186
DB 124 S1RLRCHTWNITIKVQYFQNGMKKFSHQNFHINATLKOGGSYFCGIIKNVDLS 183
QY 187 SEPLNITV 194
DB 184 SEPVKVTV 191

RESULT 10
FC3A_HUMAN
ID FC3A_HUMAN STANDARD; PRT; 254 AA.
AC P08637;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor
DE (IGG Fc receptor III-2) (Fc-gamma RIII-alpha) (Fc-gamma RIIIA)
DE (FCRIIA) (Fc-gamma RIII) (FCRII) (CD16-A) (FcR-10).
GN FCGR3A OR FCGR3 OR FCGR3 OR IFRP3 OR CD16A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=89328325; PubMed=3526846;
RA Ravetch J.V., Perussia B.;
RT "Alternative membrane forms of Fc gamma RIII (CD16) on human natural
RT killer cells and neutrophils. Cell type-specific expression of two
RT genes that differ in single nucleotide substitutions.";
RL J. Exp. Med. 170:481-497(1989).
RN [2];
RP SEQUENCE OF 1-39 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=95138131; PubMed=7836402;
RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT genes. Molecular characterization of the promoter regions.";
RL J. Biol. Chem. 270:1350-1361(1995).
RN [3];
RP VARIANTS ARG-66 AND HIS-66.
RX MEDLINE=96183251; PubMed=8609432;
RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,
RA van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;
RT "A triallelic Fc gamma receptor type IIIA polymorphism influences the
RT binding of human IgG by NK cell Fc gamma RIIIA.";
RL J. Immunol. 156:3948-3955(1996).
RN [4];
RP VARIANT VAL-157.
RX MEDLINE=97385047; PubMed=9242542;
RA Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,
RA de Haas M.;
RT "Fc gamma RIIIA-158V/F polymorphism influences the binding of IgG by
RT natural killer cell Fc gamma RIIIA, independently of the Fc
RT gamma RIIIA-48L/R/H phenotype.";
RL Blood 90:1109-1114(1997).
RN [5];
RP VARIANT VAL-176.
RX MEDLINE=97426467; PubMed=9276722;
RA Wu J., Edberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,
RA Salmon J.E., Kimberly R.P.;
RT "A novel polymorphism of Fc gamma RIIIA (CD16) alters receptor function
RT and predisposes to autoimmune disease.";
RL J. Clin. Invest. 100:1059-1070(1997).

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CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR
CC AGGREGATED IGG AND ALSO MONOMERIC IGG. MEDIATES ANTIBODY-DEPENDENT
CC CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT
CC RESPONSES, SUCH AS PHAGOCYTOSIS.
CC -!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC
CC EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (potential). Exists
CC also as a soluble receptor.
CC -!- TISSUE SPECIFICITY: Expressed on natural killer cells,
CC macrophages, subpopulation of T cells, immature thymocytes and
CC placental trophoblasts.
CC -!- PTM: Glycosylated. Contains high mannose-and complex-type
CC oligosaccharides.
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC -!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of
CC IgG1, IgG3 and IgG4 compared with isoform Phe-157. Alleles Leu-66
CC and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in
CC linkage disequilibrium.
CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:
CC FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-
CC SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE
CC DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD16A entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd16a.htm".
CC -----
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CC -----
CC EMBL; X52645; CAA36870.1; -
CC EMBL; 246222; CAA86295.1; -
CC FIR; JLO107; JLO107.
CC HSSP; PI23119; IALS.
CC Gensu; HGNC:3619; FCGR3A.
CC MIM; 146740; -
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; Ig; 2.
CC PROSITE; PS50835; IG LIKE; 2.
CC KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 16
FT CHAIN 17 254
FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT REGION RECEPTOR III-A.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 229
FT DOMAIN 230 254
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT L -> R.
FT /FTid=VAR_008799.
FT L -> H.
FT /FTid=VAR_008800.
FT F -> V.
FT /FTid=VAR_008801.
FT F -> V (in dbSNP:396991).
FT /FTid=VAR_003960.
FT /FTid=VAR_003960.
FT SEQUENCE 254 AA; 29089 MW; D38D178D32C67337 CRC64;

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DR EMBL; X73371; CAA51788.1; -;
 DR PIR; S36903; S36903.
 DR HSP; F12319; IALS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR PROSITE; PS0835; IG LIKE; 2.
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Immunoglobulin domain; Repeat.
 FT SIGNAL 1 31
 FT CHAIN 32 285
 FT DOMAIN 32 212
 FT TRANSMEM 213 233
 FT DOMAIN 234 285
 FT DOMAIN 36 118
 FT DOMAIN 119 201
 FT SITE 262 267
 FT DISULFID 59 101
 FT DISULFID 140 184
 FT CARBOHYD 67 67
 FT CARBOHYD 75 75
 FT CARBOHYD 86 86
 FT CARBOHYD 94 94
 FT CARBOHYD 168 168
 FT CARBOHYD 175 175
 SQ SEQUENCE 285 AA; 3204 MW; 255540A584CFFA0A CRC64;

Query Match 34.0%; Score 364.5; DB 1; Length 285;
 Best Local Similarity 38.9%; Pred. No. 1.e-24;
 Matches 72; Conservative 36; Mismatches 76; Indels 1; Gaps 1;
 QY 10 LLCVALLFFAPDGLVLPQPKVSLNPPNRIKGVNVTLCNGNPFVSSKTFHNGS 69
 DB 19 LLTAVLNLVAESHAGLP-KAVVLEPPHVLQVLEKEDVTLMCEGTHTKNCSTQWFNGS 77
 QY 70 LSEBNSLNLVNAKFDSEGEYKQHQOVNESEPVYLEVFSMDLLLOASAEVVMGQPLF 129
 DB 78 SIMHQAQANYTFKATVNDSDGEYRCMEETGISEPIHLGVISDWLLQLTSLVPEEGETIT 137
 QY 130 LRCHGRNWDVYKVIYKDGKALYVYENHNISITNATVDSGTGYCTGKVWOLDYSESP 189
 DB 138 LRCHSWNKQLTKVLLFQNGKPVRYHQSSNFSIPKANHSHSGNYCKAYLGRMTMVSKEP 197
 QY 190 LNIITV 194
 DB 198 VTITV 202

RESULT 13
 FC3B_HUMAN STANDARD; PRT; 233 AA.
 ID FC3B_HUMAN
 AC 075015;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor III-B precursor
 DE (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIB)
 DE (FCRIIB) (Fc-gamma RIII) (FCRII) (CD16-B) (FCR-10).
 GN FCR3B OR FC3 OR FCR3 OR IGR3 OR CD16B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (VARIANT NA-2).
 RX MEDLINE=89328325; PubMed=2526846;

RA Ravetch J.V., Perussia B.;
 RT "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
 RT killer cells and neutrophils. Cell type-specific expression of two
 RT genes that differ in single nucleotide substitutions.";
 RL J. Exp. Med. 170:461-497(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (VARIANT NA-2).
 RC TISSUE=Placenta;
 RX MEDLINE=88232937; PubMed=2967436;
 RA Simmons D., Seed B.;
 RT "The Fc gamma receptor of natural killer cells is a phospholipid-
 RT linked membrane protein";
 RL Nature 333:568-570(1988).
 RN [3]
 RP ERRATUM.
 RA Simmons D., Seed B.;
 RL Nature 340:662-662(1989).
 RN [4]
 RP SEQUENCE FROM N.A. (VARIANT NA-1).
 RC TISSUE=Leukocyte;
 RX MEDLINE=89128838; PubMed=2521732;
 RA Peltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;
 RT "Human Fc-gamma-RIII: Cloning, expression, and identification of the
 RT chromosomal locus of two Fc receptors for IgG.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).
 RN [5]
 RP SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).
 RC TISSUE=Placenta;
 RX MEDLINE=95138131; PubMed=7836402;
 RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
 RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
 RT genes. Molecular characterization of the promoter regions.";
 RL J. Biol. Chem. 270:1350-1361(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 FC.
 RX MEDLINE=20372189; PubMed=10917521;
 RA Sondermann P., Huber R., Oosthuizen V., Jacob U.;
 RT "The 3.2-A crystal structure of the human IgG1 Fc fragment-Fc
 RT gammaRIII complex.";
 RL Nature 406:267-273(2000).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.
 RX MEDLINE=20471519; PubMed=11021536;
 RA Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,
 RA Sautes-Fridman C., Sun P.D.;
 RT "Crystal structure of the extracellular domain of a human Fc gamma
 RT RIII.";
 RL Immunity 13:387-395(2000).
 RN [8]
 RP VARIANT SH ASP-78.
 RX MEDLINE=97180159; PubMed=9028335;
 RA Bux J., Stein E.L., Bierling P., Fromont P., Clay M., Stroncek D.,
 RA Santoso S.;
 RT "Characterization of a new alloantigen (SH) on the human neutrophil Fc
 RT gamma receptor IIIB.";
 RL Blood 89:1027-1034(1997).
 CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
 CC AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO
 CC MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE
 CC ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A
 CC TRAP FOR IMMUNE COMPLEXES IN THE PERIPHERAL CIRCULATION WHICH DOES
 CC NOT ACTIVATE NEUTROPHILS.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC EXISTS ALSO AS A SOLUBLE RECEPTOR, PRODUCED BY A PROTEOLYTIC
 CC CLEAVAGE.
 CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY BY POLYMORPHONUCLEAR
 CC LEUKOCYTES (NEUTROPHILS). ALSO EXPRESSED BY STIMULATED
 CC EOSINOPHILS.
 CC -!- PTM: GLYCOSYLATED. GLYCOSYLATION PLAYS AN INHIBITORY ROLE IN THE
 CC INTERACTION WITH IGG3.
 CC -!- PTM: The soluble form is produced by a proteolytic cleavage.
 CC -!- POLYMORPHISM: There are three allelic forms of FCR3B: NA-1, NA-2

CC (shown here) and SH. NA-1 and NA-2 are detectable with antibodies
 CC against the biallelic neuropil-specific antigen system NA.
 CC -!- DISEASE: the more active NA-1 allele has been associated with
 CC severe renal disease in certain systemic vasculitides.
 CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:
 CC FCGR3A AND FCGR3B (SHOWN HERE) WHICH ARE EXPRESSED IN A TISSUE-
 CC SPECIFIC MANNER. THE PHE-203 IN FCGR3A DETERMINES THE
 CC TRANSMEMBRANE DOMAINS WHEREAS THE SER-203 IN FCGR3B DETERMINES THE
 CC GPI-ANCHORING.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD16B entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd16b.htm".
 CC -----
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 CC EMBL; X07934; CAA30758.1; -;
 CC EMBL; J04162; AAA35881.1; -;
 CC EMBL; Z46223; CAA86296.1; -;
 CC PIR; J00284; J00284.
 CC PDB; 1E4J; 04-AUG-00.
 CC PDB; 1E4K; 06-JUN-01.
 CC PDB; 1EWL; 22-NOV-00.
 CC PDB; 1IIS; 16-MAY-01.
 CC PDB; 1IIX; 16-MAY-01.
 CC Genev; HGNC:3620; FCGR3B.
 CC GO; GO:0006955; P:Immune response; TAS.
 CC InterPro; IPR007110; Ig-like.
 CC Pfam; PF00047; Ig; 2.
 CC SMART; SM00409; Ig; 2.
 CC PROSITE; PSS0835; Ig-Like; 1.
 CC IGG-binding protein; Receptor; GPI-anchor; Glycoprotein; Signal;
 CC Immunoglobulin domain; Repeat; Multigene family; Polymorphism;
 CC 3D-structure; Lipoprotein.
 CC FT SIGNAL 1 16
 CC FT CHAIN 17 200
 CC
 CC FT PROPEP 201 233
 CC FT LIPID 200 200
 CC FT DOMAIN 40 96
 CC FT DOMAIN 121 179
 CC FT DISULFID 47 89
 CC FT DISULFID 128 172
 CC FT CARBOHYD 56 56
 CC FT CARBOHYD 63 63
 CC FT CARBOHYD 82 82
 CC FT CARBOHYD 92 92
 CC FT CARBOHYD 180 180
 CC FT CARBOHYD 187 187
 CC FT VARIANT 36 36
 CC
 CC FT VARIANT 65 65
 CC FT VARIANT 78 78
 CC FT VARIANT 82 82
 CC FT VARIANT 106 106
 CC
 CC FT SEQUENCE 233 AA; 26216 MW; 7AB5159432761726 CRC64;
 CC
 CC Query Match 33.9%; Score 363.5; DB 1; Length 233;
 CC Best Local Similarity 42.8%; Pred. No. 1e-24;
 CC Matches 80; Conservative 26; Mismatches 78; Indels 3; Gaps 2;
 CC
 CC 10 LLCVALLFPADGVLAQPKK--VSLNPPNWRKFGENTVLTGNNFFVSTKTFHN 67

Db 5 LLPTALLLVASAG-MRTEDLPKAVFLEFQWVSLKSDVTLKCOQAYSPEDNSTQFHN 63
 Qy 68 GSLSEETNSLNIVNAKFEDSGYKQHQVNSEPYLEVFSDFWLLLOQASAEVWEGQP 127
 Db 64 ESLISSQASSYFIDAATVNDSGYRCQTNLSTLSDPVLQEVHIGWLLLOQAPRVFKEDP 123
 Qy 128 LFLRCHGRWVDYKVIYKDGALXVWENHISITNATVEDSGTYCTGKVMQLDYES 187
 Db 124 IHLRCHSKNTALHKVYTLQNGDKRYFHNSDFHPKATLKDSGYSFCEGLVGSKNVSS 183
 Qy 188 EPLNITV 194
 Db 184 ETVNITI 190
 RESULT 14
 FCGR3 RAT
 ID _FCGR3 RAT STANDARD; PRT; 267 AA.
 AC P27645; Q04798; Q63204;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor
 DE (IgG Fc receptor III) (FC-gamma RIII) (FCRIII).
 CN FCGR3.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=91250730; PubMed=1710249;
 RA Farber D.L., Sears D.W.;
 RT "Rat CD16 is defined by a family of class III Fc gamma receptors
 RT requiring co-expression of heteroprotein subunits.";
 RL J. Immunol. 146:4352-4361(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Natural killer cells;
 RX MEDLINE=90239026; PubMed=1692135;
 RA Zeger D.L., Hogarth P.M., Sears D.W.;
 RT "Characterization and expression of an Fc gamma receptor cDNA cloned
 RT from rat natural killer cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM H).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=93246650; PubMed=8482840;
 RA Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P.,
 RA Sears D.W.;
 RT "Rat class III Fc gamma receptor isoforms differ in IgG subclass-
 RT binding specificity and fail to associate productively with rat CD3
 RT zeta.";
 RL J. Immunol. 150:4364-4375(1993).
 CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
 CC gamma. Low affinity receptor.
 CC -!- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS.
 CC THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE
 CC EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=8;
 CC Comment=Additional isoforms seem to exist;
 CC Name=C;
 CC IsoId=P27645-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=P27645-3; Sequence=Not described;
 CC Name=B;
 CC IsoId=P27645-4; Sequence=Not described;
 CC Name=D;
 CC IsoId=P27645-5; Sequence=Not described;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 30.9965 Seconds
(without alignments)
2005.293 Million cell updates/sec

Title: US-10-763-400-11

Perfect score: 1073

Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKWLQDYSEPLNITVKA 197

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	618	57.5	260	6 QSMJ20	Qsmj20 oviv aries
2	617	57.5	255	6 QSMJ30	Qsmj30 equus caball
3	383.5	35.7	357	6 QSPW5	Qspw5 macaca fasc
4	378.5	35.3	349	6 QSMZ70	Qsmz70 bos taurus
5	376	35.0	374	4 Q92663	Q92663 homo sapien
6	375.5	35.0	280	4 Q92637	Q92637 homo sapien
7	375.5	35.0	375	4 Q92495	Q92495 homo sapien
8	374.5	34.9	294	6 QSPW3	Qspw3 macaca fasc
9	373.5	34.8	330	11 QBR142	Qbr142 mus musculus
10	369.5	34.4	254	6 QSPW2	Qspw2 macaca fasc
11	367	34.2	249	11 QBR477	Qbr477 mus musculus
12	366.5	34.2	372	6 Q7YQJ5	Q7yqj5 canis faml
13	365	34.0	249	11 QBR2R4	Qbr2r4 mus musculus
14	363	33.8	249	6 Q9N216	Q9n216 felis silve
15	363	33.8	261	11 Q9ES92	Q9es92 mus musculus
16	359.5	33.5	233	4 QUPY7	Qupy7 homo sapien

17	357.5	33.3	250	6 Q9N215	Q9n215 felis silve
18	355	33.1	318	11 Q8VIQ0	Q8viq0 rattus norv
19	353	32.9	261	11 Q7TMM9	Q7tmw9 mus musculus
20	352.5	32.9	227	6 Q95N21	Q95n21 sus scrofa
21	352.5	32.9	256	6 Q95N22	Q95n22 sus scrofa
22	351.5	32.8	310	6 Q8SPW4	Q8spw4 macaca fasc
23	348.5	32.5	316	6 Q8SPV8	Q8spv8 pan troglod
24	341.5	31.8	316	4 Q8WW64	Q8ww64 homo sapien
25	337.5	31.5	316	4 Q8WJN1	Q8wun1 homo sapien
26	271.5	25.3	515	4 Q96RE0	Q96re0 homo sapien
27	269.5	25.1	199	4 Q96P27	Q96p27 homo sapien
28	267.5	24.9	189	4 Q96P28	Q96p28 homo sapien
29	267.5	24.9	535	4 Q96P75	Q96p75 homo sapien
30	267.5	24.9	639	4 Q96P30	Q96p30 homo sapien
31	267.5	24.9	734	4 Q96P31	Q96p31 homo sapien
32	267.5	24.9	734	4 Q96LA4	Q96la4 homo sapien
33	267.5	24.9	740	4 Q96P29	Q96p29 homo sapien
34	267.5	24.9	742	4 Q8N6S2	Q8n6s2 homo sapien
35	267	24.9	977	4 Q96RD9	Q96rd9 homo sapien
36	257	24.0	582	11 Q80WN2	Q80wn2 mus musculus
37	246	22.9	360	4 Q8N732	Q8n732 homo sapien
38	205	19.1	188	4 Q92638	Q92638 homo sapien
39	202.5	18.9	509	11 Q91YK7	Q91yk7 mus musculus
40	202.5	18.9	509	11 Q9EQY5	Q9eqy5 mus musculus
41	191.5	17.8	130	4 Q81ZV7	Q81zv7 homo sapien
42	187.5	17.5	365	4 Q8NEW4	Q8new4 homo sapien
43	187.5	17.5	376	4 Q8WXH3	Q8wxh3 homo sapien
44	175.5	16.4	352	11 Q920A9	Q920a9 mus musculus
45	175.5	16.4	353	11 Q8VHP5	Q8vhp5 mus musculus

ALIGNMENTS

RESULT 1

QSMJ20 PRELIMINARY; PRT; 260 AA.

AC Q8M2G0;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE High affinity immunoglobulin E receptor alpha subunit.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1; TISSUE=Bone marrow;
RX MEDLINE=20424522; PubMed=10970105;
RA McAleese S.M., Halliwell R.E.W., Miller H.R.P.;
RT "Cloning and Sequencing of the horse and sheep high-affinity IgE receptor alpha chain cDNA."
RL Immunogenetics 51:878-881(2000).
DR EMBL; Y18205; CAB40544.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGG2; 2.
DR SMART; PS50835; IGLIKE; 2.
DR PROSITE; PS50835; IGLIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 260 AA; 30047 MW; 57111F2F17D596ED CRC64;

Query Match 57.6%; Score 618; DB 6; Length 260;
Best Local Similarity 59.9%; Pred. No. 1.le-48;
Matches 115; Conservative 25; Mismatches 52; Indels 0; Gaps 0;

QY 5 MESPTLLCVALLFPAPDGVLAIPQKPKVSLNPPNWFIFKGVNLTFCNGNPFVSVSTKW 64

Db 6 MGAPALLNIALLLFSPDGMASAAWKSLSNPPWREIFRGETVTLTCGVRSSSESSVW 65
 QY 65 FINGSLSEBTNSLNIWNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAEVWME 124
 Db 66 IINGTILKTNRWDLVKAQVDSGKYOCRIKGFAPISBPVYLNVISDWLLILQASAEVWME 125
 QY 125 GQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVDSGTYYCTGKVMOLD 184
 Db 126 GESLFLRCHSWKNAFAKVIYKDNRAKLYWYENHNISITNATVDSGTYYCTGKVMOLD 185
 QY 185 YESEPINITVIX 196
 Db 186 YTSNKLKIIVK 197

RESULT 2

Q8M130
 ID Q8M130 PRELIMINARY; PRT; 255 AA.
 AC Q8M130;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE High affinity immunoglobulin E receptor alpha subunit.
 OS Equus caballus (Horse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;
 RX MEDLINE=20424522; PubMed=10970105;
 RA McLeese S.M., Halliwell R.E.W., Miller H.R.P.;
 RT "Cloning and Sequencing of the horse and sheep high-affinity IgE
 RT receptor alpha chain cDNA";
 RL Immunogenetics 51:878-881(2000).
 DR EMBL; Y18204; CAB40387.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00408; IGG2; 2.
 DR PROSITE; PS0835; IG LIKE; 2.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 255 AA; 29366 MW; A60659700684FBD8 CRC64;

Query Match 57.5%; Score 617; DB 6; Length 255;
 Best Local Similarity 60.2%; Pred. No. 1.4e-48;
 Matches 121; Conservative 24; Mismatches 52; Indels 4; Gaps 1;
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQKPKVSLNPPWNRIFKGENVTILTCGNPFVVS 60
 Db 1 MPAPMGSPALLWITFLFLSDGLGVPFAIRKSTVSLNPPWNRIFKGENVTILTCGNKPLKGN 60
 QY 61 STKWFHNGSLSEBTNSLNIWNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAE 120
 Db 61 STEWYNTTLEVTSSLTNITNASHSSGEYRCRNDNLSEAVHLEVPDMLILQASAE 120
 QY 121 VVMEGQPLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVDSGTYYCTG-- 178
 Db 121 EVIEGKALVLRCKGWKDWDFKVIYKDGKFLPYWYENKNISIESATTENSCTYYCEGAF 180
 QY 179 --KWQWLDYESEPINITVIX 197
 Db 181 NFRTSERTVSDYLNITVKA 201

RESULT 3

Q8SPW5
 ID Q8SPW5 PRELIMINARY; PRT; 357 AA.
 AC Q8SPW5;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 GN FCGR1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
 RA Presta L.G.;
 RT "Binding of human IgG to cynomolgus FcR";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF485812; AAL92095.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00409; IG; 3.
 DR PROSITE; PS0835; IG LIKE; 3.
 KW Receptor.
 SQ SEQUENCE 357 AA; 40715 MW; F5C51A06A3BCB08F CRC64;
 Query Match 35.7%; Score 383.5; DB 6; Length 357;
 Best Local Similarity 40.7%; Pred. No. 5.8e-27;
 Matches 74; Conservative 38; Mismatches 67; Indels 3; Gaps 3;
 QY 14 ALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTILTCGNPFVVSSTKWFHNGSLSE 72
 Db 6 ALLLVWPDVGQVDT-TKAVITLQPPWVSFQETVTLQCEVPLPGSSSTQWFLNGTATQ 64
 QY 73 ETNSSLNIWNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAEVWMEGQPLR 132
 Db 65 TSTPSYRITSASVSDSGEYRCQSGRSDPIQIEHRDMLLLQVSRVTEGEPLALRC 124
 QY 133 HGRNWDVYKVIYKDGKALKYWYENHNISITNATVDSGTYYCTGKVMOLDYESEPLNI 192
 Db 125 HAWKDKLVYVLYYQNGKAPKFFYNSQLTILTKNISHNGAYHCSG-MGXHYTSAGSV 183
 QY 193 TV 194
 Db 184 TV 185
 RESULT 4
 Q8MZTO PRELIMINARY; PRT; 349 AA.
 ID Q8MZTO
 AC Q8MZTO;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Fc gamma receptor 1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20349800; PubMed=1089306;
 RA Yan Y., Li X., Wang A., Zhang G.;
 RT "Molecular cloning and identification of full-length cDNA encoding
 RT high affinity Fc receptor for bovine IgG (Fc gamma RI)";
 RL Vet. Immunol. Immunopathol. 75:151-159(2000).
 DR EMBL; AF162866; AAF80477.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig_c2.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00408; IGG2; 1.

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DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 349 AA; 39608 MW; D0B77B2EF9408C02 CRC64;

Query Match 35.3%; Score 378.5; DB 6; Length 349;
Best Local Similarity 40.2%; Pred. No. 1.6e-26;
Matches 74; Conservative 38; Mismatches 71; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSL 70
Db 3 LIALILGAPVAEQVDPTKAVITLKPPWVSFQENVTLLCEGPHRPGDGTATQWFLNGTA 62
QY 71 SEETNSSLNIVNAKPEDSGEYKQCQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFL 130
Db 63 IKTLPARYSINATDSDSGEYKQCQGLNSLSDPQVLEHSDWLLQLQVTSRVFTGEGPLAL 122
QY 131 RCHGWRNDVYKVIYKDGKALKYWHENHISITNATVEDSGTYCTGKVMQLDYSEPL 190
Db 123 RCHAWKDLVNVLYYRNGKAFKFFHWNSTILKTNISHNGTYHCSG-RRRRYTSAGV 181

QY 191 NITV 194
Db 182 SVTV 185

RESULT 5
Q92663 PRELIMINARY; PRT; 374 AA.
AC Q92663;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor I.
GN Al.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Porjes A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03418; AAA36049.1; -.
DR PIR; A39878; A39878.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 374 AA; 42632 MW; D33D59398CEBA699 CRC64;

Query Match 35.0%; Score 376; DB 4; Length 374;
Best Local Similarity 39.7%; Pred. No. 3e-26;
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSL 70
Db 4 LTTLLWVPDQGVDT-TRAVITLQPPWVSFQETVTLHCEVHLHFGSSSTQWFLNGTA 62
QY 71 SEETNSSLNIVNAKPEDSGEYKQCQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFL 130
Db 63 TQTSYRITSASVNDSGEYRCQGLSGRSDPIQLIHRGWLLQLQVSSRVFMEGEPLAL 122
QY 131 RCHGWRNDVYKVIYKDGKALKYWHENHISITNATVEDSGTYCTGKVMQLDYSEPL 190
Db 123 RCHAWKDLVNVLYYRNGKAFKFFHWNSTILKTNISHNGTYHCSG-MGKRYTSAGI 181

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QY 191 NITV 194
Db 182 SVTV 185

RESULT 6
Q92637 PRELIMINARY; PRT; 280 AA.
AC Q92637;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor I.
GN B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Porjes A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03419; AAA35825.1; -.
DR PIR; A55577; A55577.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AE3D345C6 CRC64;

Query Match 35.0%; Score 375.5; DB 4; Length 280;
Best Local Similarity 41.7%; Pred. No. 2.3e-26;
Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGENVTLCNGNNFFVSVSTKWFHNGSL 70
Db 4 LTTLLWVPDQGVDT-TRAVITLQPPWVSFQETVTLHCEVHLHFGSSSTQWFLNGTA 62
QY 71 SEETNSSLNIVNAKPEDSGEYKQCQHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFL 130
Db 63 TQTSYRITSASVNDSGEYRCQGLSGRSDPIQLIHRGWLLQLQVSSRVFMEGEPLAL 122
QY 131 RCHGWRNDVYKVIYKDGKALKYWHENHISITNATVEDSGTYCTG 178
Db 123 RCHAWKDLVNVLYYRNGKAFKFFHWNSTILKTNISHNGTYHCSG 170

RESULT 7
Q92495 PRELIMINARY; PRT; 375 AA.
AC Q92495;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor type I (FC gamma RIB=FC gamma receptor).
GN CD64 OR FC<GAMMA>RIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Ravesh D.,
RA Ezekowitz A.B.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-224 FROM N.A.
RX MEDLINE=93018827; PubMed=1402657;
RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Ravesh D.P.,
RA Ezekowitz R.A.;
RT "Definition of interferon gamma-response elements in a novel human Fc
gamma receptor gene (Fc gamma Rb) and characterization of the gene
structure.";
RL J. Exp. Med. 176:1115-1123 (1992).
DR EMBL; M91555; AAA58414.1; JOINED.
DR EMBL; M91550; AAA58414.1; JOINED.
DR EMBL; M91553; AAA58414.1; JOINED.
DR EMBL; M91552; AAA58414.1; JOINED.
DR EMBL; M91553; AAA58414.1; JOINED.
DR EMBL; M91554; AAA58414.1; JOINED.
DR EMBL; M91554; AAA58414.1; JOINED.
DR EMBL; S45709; AAD13842.1; JOINED.
DR EMBL; S45708; AAD13842.1; JOINED.
DR EMBL; S45704; AAD13842.1; JOINED.
DR EMBL; S45705; AAD13842.1; JOINED.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SMC0408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 375 AA; 42881 MW; A84D46AC70DD0F91 CRC64;
Query Match 35.0%; Score 375.5; DB 4; Length 375;
Best Local Similarity 41.7%; Pred. No. 3.3e-26;
Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;
QY 11 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSTKWFHNGSL 70
DB 4 LITLLWVPGVDVT-TRAVITLQPPWVSVEQETVTLHCEVHLFGSSSTQWFLNGTA 62
QY 71 SEETNSSLINVAKPDSGEYKCOHQVNESEPPVLEVPFSDWLLLOASAEVVMGQPL 130
DB 63 TOTSTSYRITSASVNDSEYRCQGLSGRSDPIQLIHRGWLLOVSSRVFMEGEPTAL 122
QY 131 RCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMQDY 178
DB 123 RCHAWKDKLVNVLVYRNGAKKFFPHNSNLTLKTNISHNGTYHCSG 170
RESULT 8
Q8SPW3 PRELIMINARY; PRT; 294 AA.
AC Q8SPW3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor IIB.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nameruk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA Presta L.G.;
RT "Binding of human IgG to cynomolgus FcR";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485814; AAL92097.1;
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR003599; Ig.
Query Match 34.8%; Score 373.5; DB 11; Length 330;
Best Local Similarity 42.5%; Pred. No. 4.3e-26;
Matches 79; Conservative 35; Mismatches 69; Indels 3; Gaps 3;
QY 10 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSTKWFHNGS 69
DB 6 LITLLWVPGVGVNATRAVITLQPPWASIFQKENVTLMCEGPHLPDGSSTQWFINGT 65
QY 70 LSEETNSSLINVAKPDSGEYKCOHQVNESEPPVLEVP-SDWLLLOASAEVVMGQPL 128
DB 66 VQISTPSYSIVASFQDSGEYRCQIGSSVSPDPVQLIHKEDWLLLOASRRVLTEGPEL 125
QY 129 FLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMQDY 188
DB 126 ALRCHGWRNKLNVNVPYRNGKFKF-SGSKTALLKTNLSHSGIYHCSG-MGRHRYTSA 183
QY 189 PLNITV 194
DB 184 GVSITV 189

DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SMC0409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
SQ SEQUENCE 294 AA; 32151 MW; A8D476A448E3D01E CRC64;
Query Match 34.9%; Score 374.5; DB 6; Length 294;
Best Local Similarity 40.3%; Pred. No. 3e-26;
Matches 75; Conservative 32; Mismatches 78; Indels 1; Gaps 1;
QY 10 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSTKWFHNG 68
DB 29 LLTAVLFLAPVAGTPAAPPKAVLKLEPPWNLVLRSDSVLTCCGAHSPDSDTQWFHNG 88
QY 69 LSEETNSSLINVAKPDSGEYKCOHQVNESEPPVLEVPFSDWLLLOASAEVVMGQPL 128
DB 89 NLIPHTQPSYRFKANNNDSEYKCGTGRSLSDPVHLTVLSEWLAQLPHLEFREGETI 148
QY 129 FLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMQDY 188
DB 149 LLRCHSWKDKPLIKVTFPQNGISKKFSHMNPFSIPOAHSHSGDYHCTGNIGTYFSK 208
QY 189 PLNITV 194
DB 209 PVTITV 214
RESULT 9
Q8R142 PRELIMINARY; PRT; 330 AA.
AC Q8R142
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025535; AAH25535.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; IG_C2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SMC0408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein; Immunoglobulin domain.
FT NON TER 1
SQ SEQUENCE 330 AA; 891F8724F870D88E CRC64;
Query Match 34.8%; Score 373.5; DB 11; Length 330;
Best Local Similarity 42.5%; Pred. No. 4.3e-26;
Matches 79; Conservative 35; Mismatches 69; Indels 3; Gaps 3;
QY 10 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSTKWFHNGS 69
DB 6 LITLLWVPGVGVNATRAVITLQPPWASIFQKENVTLMCEGPHLPDGSSTQWFINGT 65
QY 70 LSEETNSSLINVAKPDSGEYKCOHQVNESEPPVLEVP-SDWLLLOASAEVVMGQPL 128
DB 66 VQISTPSYSIVASFQDSGEYRCQIGSSVSPDPVQLIHKEDWLLLOASRRVLTEGPEL 125
QY 129 FLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMQDY 188
DB 126 ALRCHGWRNKLNVNVPYRNGKFKF-SGSKTALLKTNLSHSGIYHCSG-MGRHRYTSA 183
QY 189 PLNITV 194
DB 184 GVSITV 189